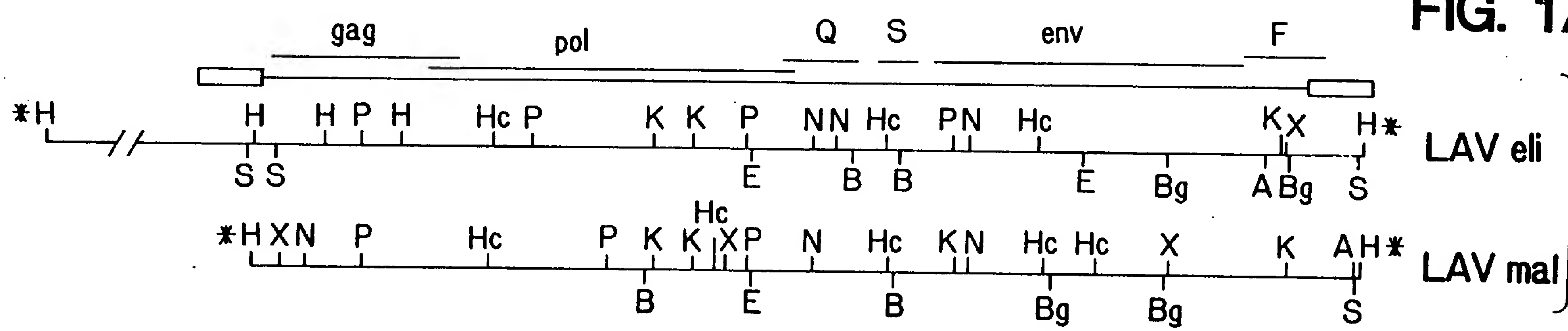
FIG. 1A


gag
pol
Q
S
env
F
*H
H H P H Hc P K K P NN Hc PN Hc KX H*
S S E B B E Bg A Bg S
LAV eli
H X N P Hc P K K Hc X P N Hc K N Hc Hc X K A H
B E B Bg Bg S
LAV mal

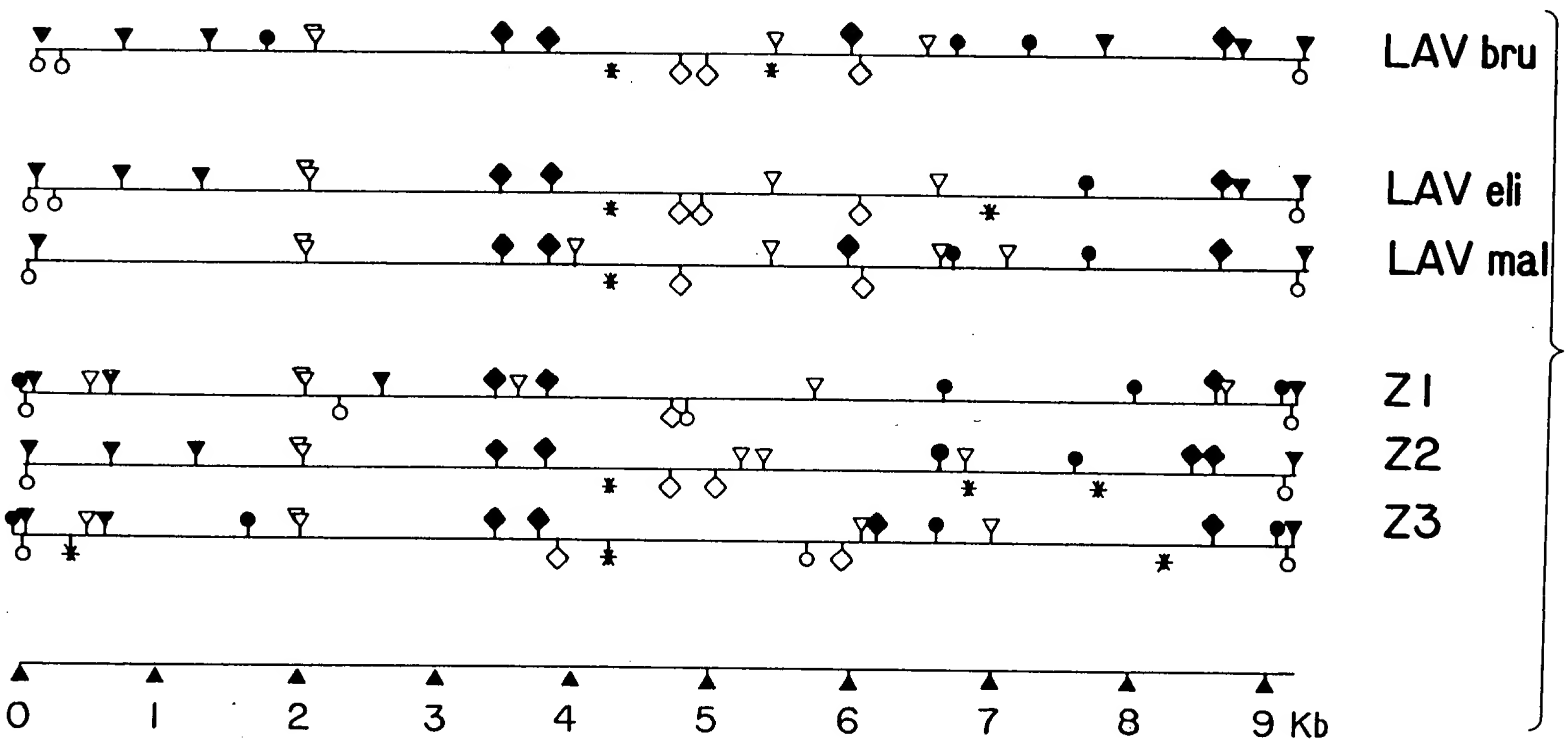
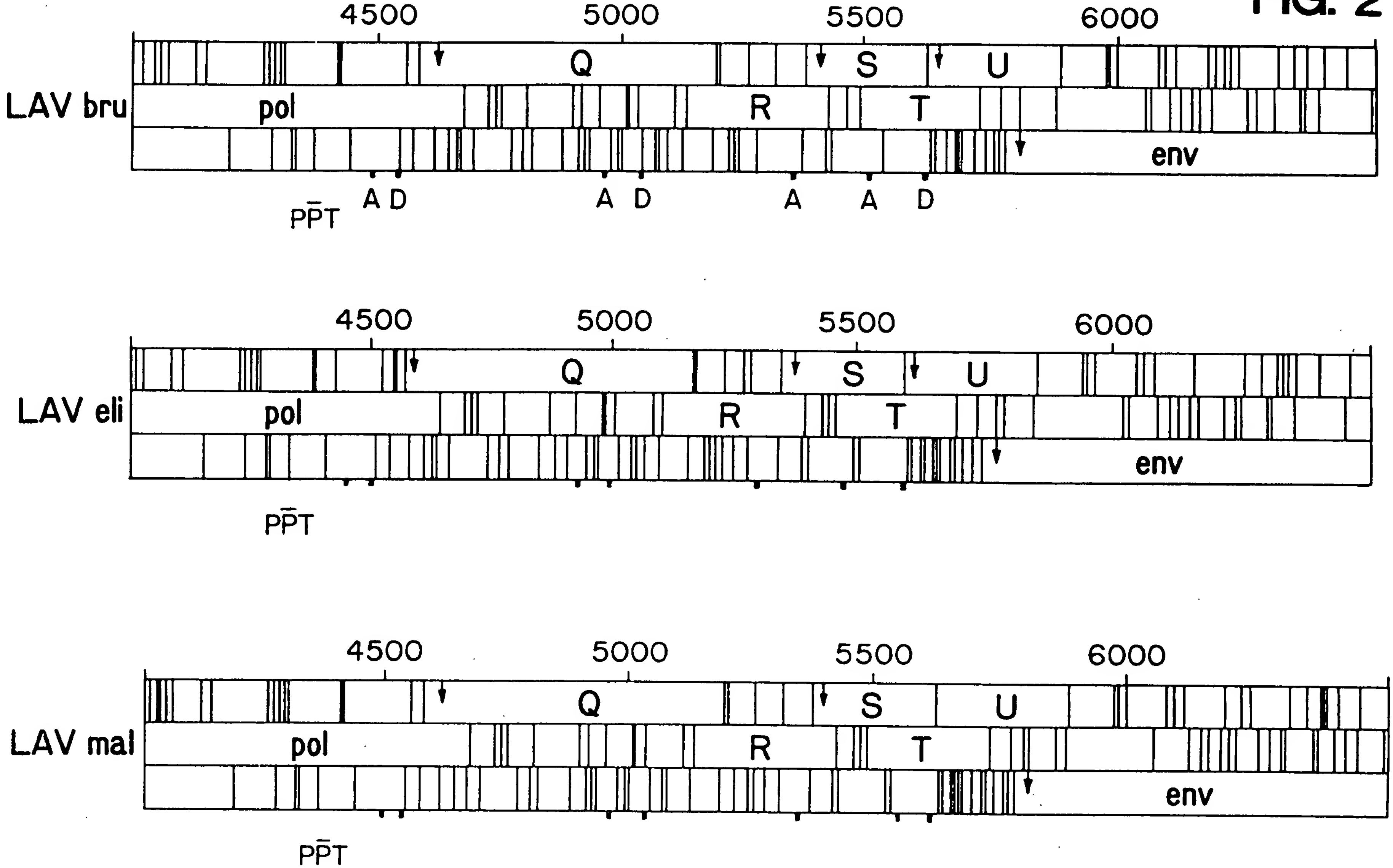


FIG. 1B

FIG. 2



4500
5000
5500
6000
LAV bru
LAV eli
LAV mal
pol
env
Q
R
S
T
U
A
D
PP̄T

GAG

```
                  10         20         30         40         50         60         70         80
LAV BRU   MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                    K
LAV MAL              K   A             R     L              L      C   Q  ME   ST K      IK
LAV ELI              K   K             R                   Y L          K   I    AI    T

                                                                  |p25
                                                                  ↓
                  90        100        110        120        130        140        150        160
LAV BRU   TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGH SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                   DV        E                   ----AAG  N              L
LAV MAL                 DV                 I     RQ T  AQQAAAA KN   S           A     I
LAV ELI            K G  DV        E M                 ------   N N              L

                 170        180        190        200        210        220        230        240
LAV BRU   WVKVVEEKAF SPEVIPMFSA LSCGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDK VHPVHAGPIA PGQMREPRGS
ARV 2
LAV MAL       I                           M   I            D        D            P
LAV ELI       I                                                           L

                 250        260        270        280        290        300        310        320
LAV BRU   DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                          D
LAV MAL                    S      D                   V                      F        T
LAV ELI                 A  S                 V        V                                        D
```

FIG. 3A-1

```
                                                                           p13
                                                                          ↓
                330        340        350        360        370        380        390        400
LAV BRU  NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                                   P-  N              T
LAV MAL                             G                  S             A  T   A         KG - RI
LAV ELI                             Q                  S             A  V  T A        KGP   I

                410        420        430        440        450        460        470        480
LAV BRU  NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPEE
ARV 2             K             R  R
LAV MAL         L                                            H                    ---- --------
LAV ELI           K             R       L              R    H                    ---- --------A

                490        500        510
LAV BRU  SFRSGVETTT PSQKQEPIDK ELYPLTSLRS LFGNDPSSQ
ARV 2       F E K
LAV MAL    GF E IK-       QK        A  K       QL
LAV ELI    GF E I -       QK           K        L
```

FIG. 3A–2

Central Region: Q

```
                  10         20         30         40         50         60         70         80
LAV BRU   MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG DARLVITTYW GLHTGERDWH
ARV 2                                      I K  K           T    V            K               E
LAV MAL                          H           K  KN          R  K V               VR      Q   K
LAV ELI                      K               K  NR             K V           E     K           E

                  90        100        110        120        130        140        150        160
LAV BRU   LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK
ARV 2          A       K        G        H       E    KN I YR                                  T
LAV MAL     H        Q      L   D                E     Q I          D                  T   A  TR
LAV ELI               R         G       M        E       I D                           T   A  Q

                 170        180        190
LAV BRU   PPLPSVTKLT EDRWNKPQKT KGHRGSHTMN GH
ARV 2           K
LAV MAL         R            Q
LAV ELI         R            Q  R
```

FIG. 3B-1

```
                R

                    10         20         30         40         50         60         70         80
LAV BRU   MEQAPEDQGP QREPHNEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                    Y             R          P   S   Y                                Q
LAV MAL        A                       Q              S                E        S          Q
LAV ELI        A         Y   A         S              S                V                   Q

                    90
LAV BRU   IGVTQQRRAR -NGASRS
ARV 2       II       R
LAV MAL     I R      -  S
LAV ELI     IIR      -  S

               S (tat)
                    10         20         30         40         50         60         70
LAV BRU   MEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2           N            R     NN         YA   R G                   A   D     A
LAV MAL     D   N      N     R  P  NK      Y    M  I  G                      N A  DP P E
LAV ELI     D   N      N     R  P  NK H    Y   P   LN G                 G    G A   PIP
```

FIG. 3B–2

POL

```
                  10         20         30         40         50         60         70         80
LAV BRU   FFREDLAFLQ GKAREFSSEQ TRANSPTFSS EQTRANSPTR RELQVWGRDN NSLSEAGADR QGTVSFNFPQ ITLWQRPLVT
ARV 2                                  --- ----------        GE
LAV MAL       N   P        P           --- ---------S    R   G - KT   T  E              I   S            V
LAV ELI       N   P     G L PK         --- ---------S    R     -  P  KT  E                                  A

                  90        100        110        120        130        140        150        160
LAV BRU   IKIGGQLKEA LLDTGADDTV LEEMSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2      R                        N   K                        PV
LAV MAL   VRV                      IN   K                              K      I              M
LAV ELI                             N   K                        P     Q

                 170        180        190        200        210        220        230        240
LAV BRU   IGCTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV MAL                               R                T   KD        L
LAV ELI                                                T    D         R           I

                 250        260        270        280        290        300        310        320
LAV BRU   LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2                                                         K
LAV MAL     N
LAV ELI                                                                S
```

FIG. 3C-1

```
                330        340        350        360        370        380        390        400
LAV BRU  KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2                                                                       F
LAV MAL                      T K  E                                 E   K   F
LAV ELI                           EM                             K  E       F R

                410        420        430        440        450        460        470        480
LAV BRU  LHPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                M                            A     K
LAV MAL              Q  D E                             K         A   DIV     A
LAV ELI           S  K    E         N ER

                490        500        510        520        530        540        550        560
LAV BRU  VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARTRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2      E          V                                  M                   VS          I
LAV MAL                                     QY           IKS                  AQ             R
LAV ELI                         H                        M            A     R S         R    R
```

FIG. 3C–2

```
                 570        580        590        600        610        620        630        640
LAV BRU   QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAASRETKLG KAGYVTNRGR QKVVTLTDTT
ARV 2           A  M                                              N             D    SIA
LAV MAL         A                                T                N    K        D    S  E
LAV ELI            A                                I             N             D    P

                 650        660        670        680        690        700        710        720
LAV BRU   NQKTELQAIH LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QIIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                      S
LAV MAL                  S                             I         Q D      S
LAV ELI            N

                 730        740        750        760        770        780        790        800
LAV BRU   AGIRKVLFLD GIDKAQDEHE KYHSNWRAMA SDFNLPPVVA KEIVASCDKC QLKGEAMHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2              N      E                                                                I
LAV MAL   S               E                    I                                           I
LAV ELI   Q               E       N

                 810        820        830        840        850        860        870        880
LAV BRU   LVAVHVASGY IEAEVIPAET GQETAYFLLK LAGRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
ARV 2
LAV MAL   I                        I          VV              AA         N
LAV ELI                                       VV              AA
```

FIG. 3D-1

```
                890        900        910        920        930        940        950        960
LAV BRU  MNKELKKIIG QVRDQAEHLK TAVQMAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSRDP
ARV 2      N
LAV MAL                E                                    IM                              KK
LAV ELI                                       RR            I       I                       N

                970        980        990       1000       1010
LAV BRU  LWKGPAKLLW KGEGAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED
ARV 2
LAV MAL  I                                                    G G
LAV ELI  I                     K          V
```

FIG. 3D-2

ENV

```
                        SP                                       OMP

              10         20         30         40         50         60         70         80
                                          •↓                               •                   •
LAV BRU  MRVK---EKY QHLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2     K  GTRRN             --- - L    M                                 R
LAV MAL      REIQRN  NW        --- -M     M  T   IA D                        S E        I
LAV ELI       ARGIERN[C] NW K  --- -I        T    ADN                         S E   A    I

              90        100        110        120        130        140        150        160
                                                     •          •     •
LAV BRU  DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-CN ATNTNSSNTN SSSGEMMME-
ARV 2             C             N      Q                        T N    - K        --- ----NWKE I
LAV MAL        IE E      G      N                               T N  NVN T  V GTNACS  RTNA LK  I
LAV ELI        IA E             N                               T N S E--L RN GTMG NV TTEEKG----

             170        180        190        200        210        220        230        240
                   •                                             •         •                 •
LAV BRU  KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                T    D I     N L RN  VV     AS T TNYTN R IN   R                       T
LAV MAL  -  V         TPVGSD R  -    T  N  LVQ   DSDN  ----S R IN                 T D
LAV ELI  ---M        VT VLKD K  QV   L  R    V     SST -NSTN R IN     A

             250        260        270        280        290        300        310        320
           •             •          •                                                    •
LAV BRU  LKCNKKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2                K                I                    D     N              E  A
LAV MAL      D K       EI K          K                  IM   E  L   T N         ET T       G   R
LAV ELI     RD K                                          I   E  L N   N    AH   E  K T  A  YQ   Q
```

FIG. 3E-1

```
                330        340        350        360        370        380        390        400
                                  •                                                          •
LAV BRU  SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT HSFNCGGEFF
ARV 2      Y --       W T RI   DI K         Q  N  E   VK             - V N          M
LAV MAL  G HF--   Q  LY T I-V  DI R Y T N ETE DK  Q  V V  GSLL- -   K   NS        T      R
LAV ELI  RTP -- L Q SLY TKS-RS IIG          Q SK  Q  V R  GTLL- -   I K  P        T      R

                410        420        430        440        450        460        470        480
                                               •                                 •
LAV BRU  YCNSTQLFNS TWFNSTWSTE CSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
ARV 2       T     N   -----RLN RTEG K N    I       I                  C   S                T -V
LAV MAL     TSK       Q NGARL- -  S  STGS          I      KT          A V N L        I       NSSD
LAV ELI     TSG       NI A NNI TES NSTNTN    Q     I  K VAGR-   I          ERN  L                   I --

                                                                                TMP
                490        500        510        520        530↓       540        550        560
LAV BRU  NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GARSMTLTVQ
ARV 2    T DT V                       I      I                      V  M               V L
LAV MAL   SDN TL            I          R                    E      I L-  M               A L
LAV ELI   STN T                        Q          R         E      I L-  M                   V
```

FIG. 3E-2

```
                570        580        590        600        610        620        630        640
                                                                       •      •
LAV BRU  ARQLLSGIVQ QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW NASWSNKSLE
ARV 2                                              W        R
LAV MAL                                            W        Q   R   M       H    F     S    R  D
LAV ELI      M                                                              H    N     S    R  N

                650        660        670        680        690        700        710        720
LAV BRU  QIWNNMTWME WDREINNYTS LINSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2    D  D     Q  E   D   N T YT L                              S
LAV MAL  D        Q  EK  S   G I YN       I      K                 S SK      R    IV    I    I
LAV ELI  E  Q        E   D   G   Y        T      K                 S  Q            I    I

                730        740        750        760        770        780        790        800
                                                                               •
LAV BRU  VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PEGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                        R   V    -    D               V    D F     E           R
LAV MAL     L             L  L        P               QG G         FS         N                AA
LAV ELI     L                L   A    -      T         G    V  L   FS                       I  AV

                810        820        830        840        850        860        870
LAV BRU  RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2     T  I  K           S      I          W         T          A R Y    L  H          L
LAV MAL                  L        G        I    T        C       IG RFG    L          F  A
LAV ELI              DI   L            R    S  FD I               II R    VLN            S
```

FIG. 3F–1

F

```
                   10         20         30         40         50         60         70         80
LAV BRU  MGGKWSKSSV VGWPTVRERM R----RAEPA ADGVGAASR- ----DLEKUG AITSSNTAAT NAACAWLEAQ EE-EEVGFPV
ARV 2          R M  G   SAI       RAEP                V  -  ----                      D          -
LAV MAL           I       KI    I  ----  TP  T  ET     V  QD  AVSQ   D  C    AA   SP   N    S ---  PP    E
LAV ELI           I       AI    I  ----  TM            V   -  ----                     S     D           SD

                   90        100        110        120        130        140        150        160
LAV BRU  TPQVPLRRHT YKAAVDLSHF LKEKGGLEGL IHSQRRQDIL DLWIYUTQGY FPDWQNYTPC PGVRYPLTFG WCYKLVPVEP
ARV 2    R                L  I              W      E                                I          F
LAV MAL  R              G F              D   VW PK   E      V                       I  F       F     HS
LAV ELI  R              E L                   W KK   E      V  N    I                I            E    D

                  170        180        190        200        210
LAV BRU  DKVEEANKGE NTSLLHPVSL HGMDDPEREV LEWRFDSRLA FHHVARELHP EYFKNC
ARV 2    E        E   N       M     E  A  K  V     K       M         Y D
LAV MAL  EE       E   NC      I  Q   E  A       K  K    S    LR  R     Q   Y D
LAV ELI  QE    DTE   TN       ICQ    E      Q   K     N       E  K    M   FY  -
```

FIG. 3F–2

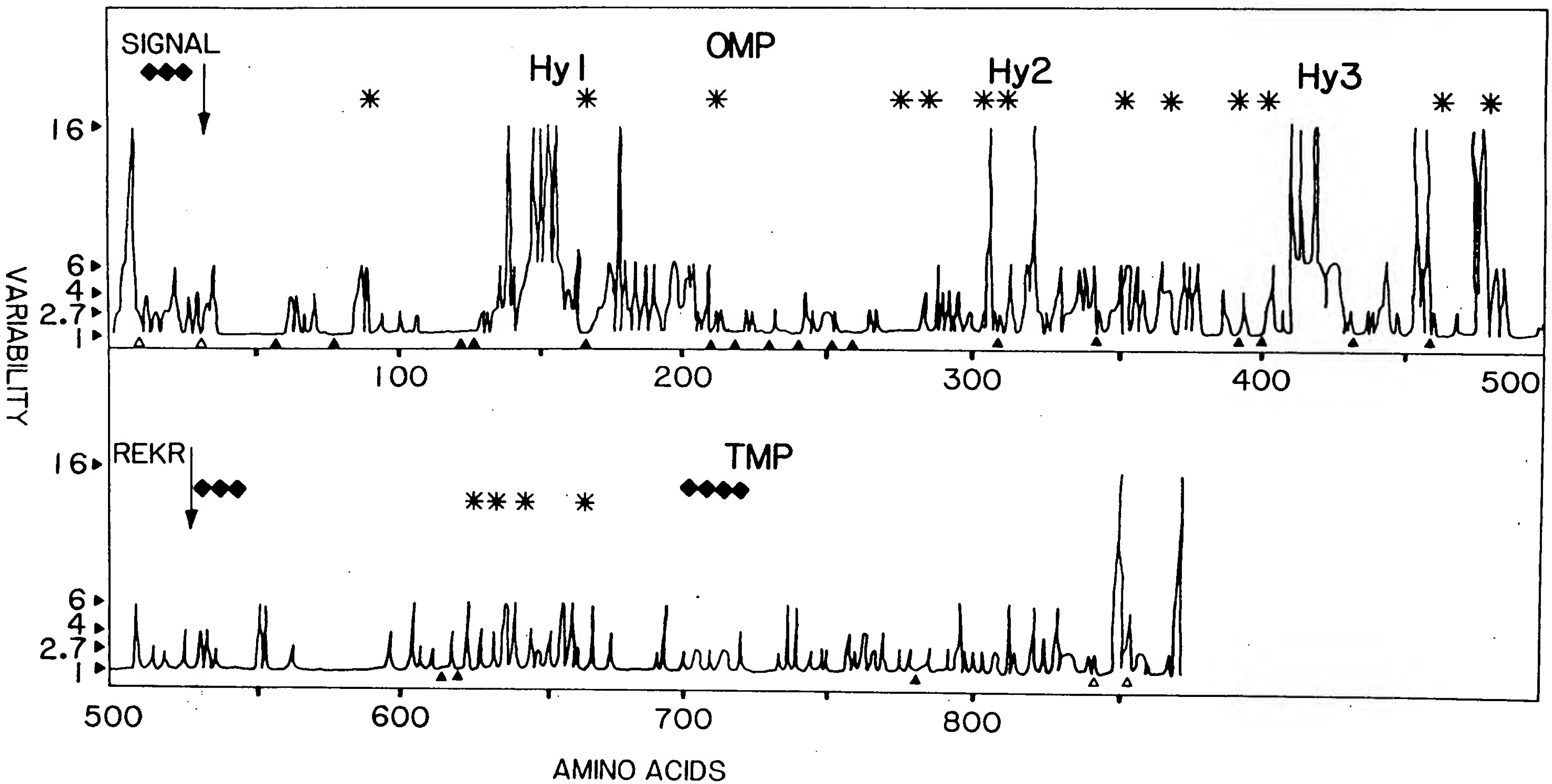
FIG. 4A

A LAVbru vs.	GAG		POL		ENV TOTAL		ENV OMP		ENV TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli ZAIRE	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal ZAIRE	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9
B LAVeli vs.										
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4B

A LAVbru vs.	orf F		central region orf Q		orf R		orf S	
HTLV-3 USA	206 0/0	1.5	192 0/0	0		nd	80 0/0	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli ZAIRE	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal ZAIRE	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8
B LAVeli vs.								
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3

FIG. 5



SIGNAL
OMP
Hy I
Hy2
Hy3
REKR
TMP
VARIABILITY
16
6
4
2.7
1
100
200
300
400
500
600
700
800
AMINO ACIDS

GAG

a

```
                                  120
            K    A    Q    Q    A    A    A                                     D    T
LAV.BRU    AAA  GCA  CAG  CAA  GCA  GCA  GCT    -    -    -    -    -          GAC  ACA

            K    A    Q    Q    A    A    A    A    A   -    -    -    -        G    T
ARV 2      AAG  GCA  CAG  CAA  GCA  GCA  GCT  GCA  GCT                         GGC  ACA

            K    T    Q    Q    A    A    A    A    Q    Q    A    A    A    A    T
LAV.MAL    AAG  ACA  CAG  CAG  GCA  GCA  GCT  GCA  CAG  CAG  GCA  GCA  GCT  GCC  ACA

            X    A    Q    Q    A    A    A                                     D    T
LAV.ELI    AAG  GCA  CAG  CAA  GCA  GCA  GCT -    -    -    -    -    -        GAC  ACA
```

FIG. 6A-1

b

```
LAV.BRU
                                   460                                            470                                               480
 G   N  | F   L   Q   S   R   P   E   P   T   A   P   P  | F   L   Q   S   R   P   E   P   T   A   P   P  | E   E
GGG AAT |TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA |TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA | GAA GAG

ARV 2
 G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                     E   E
GGG AAT TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -   GAA GAG

LAV.MAL
 G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                     A   E
GGG AAT TTC CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -   GCA GAG

LAV.ELI
 G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                     A   E
GGG AAC TTT CTC CAA AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -   GCA GAG
```

FIG. 6A–2

c

			20									30
LAV.BRU	R AGA	M ATG	R AGA	-	-	-	-	R CGA	A GCT	E GAG	P CCA	A GCA
ARV 2	R AGA	M ATG	R AGA	R CGA	A GCT	E GAG	P CCA	R CGA	A GCT	E GAG	P CCA	A GCA
LAV.MAL	R AGA	I ATA	R AGA	-	-	-	-	R CGA	T ACT	P CCC	P CCA	T ACA
LAV.ELI	R AGA	I ATA	R AGA	-	-	-	-	R AGA	T ACT	P AAT	P CCA	T GCA

d

					40							
LAV.BRU	V GTG	G GGA	A GCA	A GCA	S TCT	R CGA	-	-	-	-	-	D GAC
ARV 2	V GTG	G GGA	A GCA	V GTA	A TCT	R CGA	-	-	-	-	-	D GAC
LAV.MAL	V GTA	G GGA	A GCA	V GTA	S TCT	R CAA	D GAT	A GCA	V GTA	S TCT	Q CAA	D GAT
LAV.ELI	V GTA	G GGA	A GCA	V GTA	S TCT	R CGA	-	-	-	-	-	D GAC

FIG. 6A-3

ENV

e

```
                                               20
            Q   H   L    W   R   W   G     W   K   W   G     T   M   L
LAV.BRU    CAG CAC TTG [TGG ACA TGG GGC] [TGG AAA TGG GGC]  ACC ATG CTC

            Q   H   L   W   R   W   G                        T   L   L
ARV 2      CAG CAC TTG TGG AGA TGG GGC   -   -   -   -       ACC TTG CTC

            Q   N   W   W   R   W   G                        M   M   L
LAV.MAL    CAA AAC TGG TGG AGA TGG GGC   -   -   -   -       ATG ATG CTC

            Q   N   W   W   K   W   G                        T   M   L
LAV.ELI    CAA AAC TGG TGG AAA TCG GGC   -   -   -   -       ATC ATG CTC
```

FIG. 6B-1

f

```
LAV.BRU                         140                                        150
 L   K   C   T   D   L       G   N   A   T    N   T   N   S   S     N   T   N   S   S    S   G   E
TTA AAG TGC ACT GAT TTG  -  GGG AAT GCT ACT [AAT ACC AAT AGT AGT] [AAT ACC AAT AGT AGT] AGC GGG GAA
 M   M   M   E       K   G   E   I
ATG ATG ATG GAG  -  AAA GCA GAG ATA

ARV 2
 L   N   C   T   D   L       G   K   A   T   N   T   N   S   S                                 M
TTA AAT TGC ACT GAT TTG  -  GGG AAG GCT ACT AAT ACC AAT AGT AGT  -   -   -   -   -   -   -   AAT
 W    K   E   E   I     K   G   E   I
TGG [AAA GAA GAA ATA] [AAA GGA GAA ATA]
```

LAV.MAL

```
 L   N   C   T   N   V   N   G   T   A   V   N   G   T   N   A   G   S   N   R   T   N   A   E
TTA AAC TGC ACT|AAT GTG AAT GGG ACT|GCT GTG AAT GGG ACT|AAT GCT GGG|AGT AAT AGG ACT AAT GCA GAA|
 L   K   M   E   I       G   E   V
TTG AAA ATG GAA ATT  -  GGA GAA GTG
```

LAV.ELI

```
 L   N   C   S   D   E           L   R   N   N   G   T   M   G   N   N   V   T   T   E   E   K
TTA AAC TGT AGT GAT GAA  -   -  |TTG AGG AAC AAT GGC ACT|ATG GGG AAC AAT GTC ACT|ACA GAG GAG AAA
 G                               M
GGA  -   -   -   -   -   -   -  ATG
```

FIG. 6B–2

```
g                                  200
              D   N   D   T   T   S                       Y   T   L
LAV.BRU      GAT AAT GAT ACT ACC AGC -   -   -   -   -   TAT ACG TTG

              D   N   A   S   T   T   T   N   Y   T   N   Y   R   L
ARV 2        GAT AAT GCT AGT ACT ACT ACC AAC TAT ACC AAC TAT AGG TTG

              D   D   S   D   N   S   S                   Y   R   L
LAV.MAL      GAT GAT AGT GAT AAT AGT AGT -   -   -   -   TAT AGG CTA

              D   N   D   S   S   T       N   S   T   N   Y   R   L
LAV.ELI      GAC AAT GAT AGT AGT ACC  -  AAT AGT ACC AAT TAT AGG TTA
```

FIG. 6B-3

```
h
LAV.BRU
                             410                                420                 430
 C   N   S   T   Q   L   F   N   S   T   W   F   N   S   T   W   S   T   E   G   S   N   N   T   E   G
TGT AAT TCA ACA CAA CTG TTT AAT AGT ACT TGG TTT AAT AGT ACT TGG AGT ACT GAA GGG TCA AAT AAC ACT GAA GGA
 S   D   T   I
AGT GAC ACA ATC

ARV 2
 C   N   T   T   Q   L   F   N   N   T   W                       R   L   N   H   T   K   G   T   K   G
TGT AAT ACA ACA CAA CTG TTT AAT AAT ACA TGG -   -   -   -   -   AGG TTA AAT CAC ACT GAA GGA ACT AAA GGA
 N   D   T   I
AAT GAC ACA ATC
```

```
LAV.MAL

 C   N   T   S   K   L   F   N   S   T   W   Q   N   N   G   A   R   L           S   N   S   T   E   S
TGT AAT ACA TCA AAA CTG TTT AAT AGT ACA TGG CAG AAT AAT GGT GCA AGA CTA  -   -  AGT AAT AGC ACA GAG TCA
 T   G   S   I
ACT GGT AGT ATC

LAV.ELI

 C   N   T   S   G   L   F   N   S   T   W   N   I   S   A   W   N   N   I   T   E   S   N   N   S   T
TGT AAT ACA TCA GGA CTG TTT AAT AGT ACA TGG AAT ATT AGT GCA TGG AAT AAT ATT ACA GAG TCA AAT AAT AGC ACA
 N   T   N   I
AAC ACA AAC ATC
```

FIG. 6B–4

LAV.MAL

```
→R
GGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGCAAGGAACCCACTG
                                   R←→U5
CTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAAGCAGTGTGTGCCCATCTGTTGTGT
                                      100                U5←
GACTCTGGTAACTAGAGATCCCTCAGACCACTCTAGACGGTGTAAAAATCTCTAGCAGTG

GCGCCCGAACAGGGACTTTAAAGTGAAAGTAACAGGGACTCGAAAGCGGAAGTTCCAGAG
                200
AAGTTCTCTCGACGCAGGACTCGGCTTGCTGAGGTGCACACAGCAAGAGGCGAGAGCGGC
                                                →GAG   300
                                                MetGlyAlaArg
GACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAG

 AlaSerValLeuSerGlyGlyLysLeuAspAlaTrpGluLysIleArgLeuArgProGly
AGCGTCAGTATTAAGCGGGGGAAAATTAGATGCATGGGAGAAAATTCGGTTAAGGCCAGG
                                       400
 GlyLysLysLysTyrArgLeuLysHisLeuValTrpAlaSerArgGluLeuGluArgPhe
GGGAAAGAAAAAATATAGACTGAAACATTTAGTATGGGCAAGCAGGGAGCTGGAAAGATT

 AlaLeuAsnProGlyLeuLeuGluThrGlyGluGlyCysGlnGlnIleMetGluGlnLeu
CGCACTTAACCCTGGCCTTTTAGAAACAGGAGAAGGATGTCAACAAATAATGGAACAGCT
                500
 GlnSerThrLeuLysThrGlySerGluGluIleLysSerLeuTyrAsnThrValAlaThr
ACAATCAACTCTCAAGACAGGATCAGAAGAAATTAAATCATTATATAATACAGTAGCAAC
                                                         600
 LeuTyrCysValHisGlnArgIleAspValLysAspThrLysGluAlaLeuAspLysIle
CCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACCAAGGAAGCGCTAGATAAAAT

 GluGluIleGlnAsnLysSerArgGlnLysThrGlnGlnAlaAlaAlaAlaGlnGlnAla
AGAGGAAATACAAAATAAGAGCAGGCAAAAGACACAGCAGGCAGCAGCTGCACAGCAGGC
                                         700
 AlaAlaAlaThrLysAsnSerSerSerValSerGlnAsnTyrProIleValGlnAsnAla
AGCAGCTGCCACAAAAAACAGCAGCAGTGTCAGTCAAAATTACCCCATAGTGCAAAATGC

 GlnGlyGlnMetIleHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysVal
ACAAGGGCAAATGATACATCAGGCCATATCACCTAGGACTTTGAATGCATGGGTGAAAGT
                800
 IleGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeuSerGluGly
AATAGAAGAAAAGGCTTTCAGCCCAGAAGTGATACCCATGTTCTCAGCATTATCAGAGGG
                                                         900
 AlaThrProGlnAspLeuAsnMetMetLeuAsnIleValGlyGlyHisGlnAlaAlaMet
GGCCACCCCACAAGATTTAAATATGATGCTGAACATAGTTGGAGGACACCAGGCAGCTAT

 GlnMetLeuLysAspThrIleAsnGluGluAlaAlaAspTrpAspArgValHisProVal
GCAAATGTTAAAAGATACCATCAATGAGGAAGCTGCAGACTGGGACAGGGTACATCCAGT
                                        1000
 HisAlaGlyProIleProProGlyGlnMetArgGluProArgGlySerAspIleAlaGly
ACATGCAGGGCCTATTCCCCCAGGCCAGATGAGAGAACCAAGAGGAAGTGACATAGCAGG
```

FIG. 7A

```
ThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrSerAsnProProIleProVal
AACTACTAGTACCCTTCAAGAACAAATAGGATGGATGACAAGCAACCCACCTATCCCAGT
        1100
GlyAspIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSer
GGGAGACATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAATGTATAG
                                                        1200
ProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAspTyrValAsp
CCCTGTCAGCATTTTGGACATAAGACAAGGGCCAAAGGAACCTTTTAGAGACTATGTAGA

ArgPhePheLysThrLeuArgAlaGluGlnAlaThrGlnGluValLysAsnTrpMetThr
TAGGTTCTTTAAAACTCTCAGAGCTGAGCAAGCTACACAGGAGGTAAAAAATTGGATGAC
                                    1300
GluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGly
AGAAACCTTGCTGGTCCAAAATGCGAATCCAGACTGTAAGACCATTTTAAAAGCATTAGG

ProGlyAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProSerHis
ACCAGGGGCTACATTAGAAGAAATGATGACAGCATGCCAGGGAGTGGGAGGACCCAGTCA
        1400
LysAlaArgValLeuAlaGluAlaMetSerGlnAlaThrAsnSerThrAlaAlaIleMet
TAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAACAAATTCAACTGCTGCCATAAT
                                                        1500
MetGlnArgGlyAsnPheLysGlyGlnLysArgIleLysCysPheAsnCysGlyLysGlu
GATGCAGAGAGGTAATTTTAAGGGCCAGAAAAGAATTAAGTGTTTCAACTGTGGCAAAGA

GlyHisLeuAlaArgAsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLys
AGGACACCTAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGAA
                                    1600  →POL
                                          PhePheArgGluAsnLeu
GluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrp
GGAAGGACACCAAATGAAAGACTGCACTGAGAGACAGGCTAATTTTTTAGGGAAAATTTG

AlaPheProGlnGlyLysAlaArgGluPheProSerGluGlnThrArgAlaAsnSerPro
 ProSerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaPro
GCCTTCCCACAAGGGAAGGCCAGGGAATTTCCTTCAGAGCAGACCAGAGCCAACAGCCCC
        1700
ThrSerArgGluLeuArgValTrpGlyGlyAspLysThrLeuSerGluThrGlyAlaGlu
 ProAlaGluSerPheGlyPheGlyGluGluIleLysProSerGlnLysGlnGluGlnLys
ACCAGCAGAGAGCTTCGGGTTTGGGGAGGAGATAAAACCCTCTCAGAAACAGGAGCAGAA
                                                        1800
ArgGlnGlyIleValSerPheSerPheProGlnIleThrLeuTrpGlnArgProValVal
 AspLysGluLeuTyrProLeuAlaSerLeuLysSerLeuPheGlyAsnAspGlnLeuSer
AGACAAGGAATTGTATCCTTTAGCTTCCCTCAAATCACTCTTTGGCAACGACCAGTTGTC
GAG←
ThrValArgValGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyAlaAspAspThr
 Gln
ACAGTAAGAGTAGGAGGACAGCTAAAAGAAGCTCTATTAGACACAGGAGCAGATGATACA
                                    1900
ValLeuGluGluIleAsnLeuProGlyLysTrpLysProLysMetIleGlyGlyIleGly
GTATTAGAAGAAATAAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGA

GlyPheIleLysValArgGlnTyrAspGlnIleLeuIleGluIleCysGlyLysLysAla
GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCT
        2000
```

FIG. 7B

```
IleGlyThrIleLeuValGlyProThrProValAsnIleIleGlyArgAsnMetLeuThr
ATAGGTACAATATTGGTAGGACCTACACCTGTCAACATAATTGGACGAAATATGTTGACT
                                                        2100
GlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValProValLysLeu
CAGATTGGTTGTACTTTAAATTTTCCAATTAGTCCTATTGAGACTGTACCAGTAAAATTA

LysProGlyMetAspGlyProArgValLysGlnTrpProLeuThrGluGluLysIleLys
AAGCCAGGGATGGATGGCCCAAGGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA
                                        2200
AlaLeuThrGluIleCysLysAspMetGluLysGluGlyLysIleLeuLysIleGlyPro
GCATTAACAGAAATTTGTAAAGATATGGAAAAGGAAGGAAAAATTTTAAAAATTGGGCCT

GluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSerThrLysTrpArg
GAAAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGCACTAAATGGAGA
                2300
LysLeuValAsnPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluValGlnLeu
AAATTAGTGAATTTCAGAGAGCTTAATAAAAGAACTCAAGATTTTTGGGAAGTTCAATTA
                                                        2400
GlyIleProHisProAlaGlyLeuLysLysLysLysSerValThrValLeuAspValGly
GGAATACCACATCCTGCTGGGTTGAAAAAGAAAAAATCAGTCACAGTATTGGATGTGGGG

AspAlaTyrPheSerValProLeuAspGluAspPheArgLysTyrThrAlaPheThrIle
GATGCATATTTTTCAGTCCCTTTAGATGAAGATTTCAGGAAGTATACTGCATTCACTATA
                                        2500
ProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnValLeuProGlnGly
CCCAGTATTAATAATGAGACACCAGGGATTAGATATCAGTACAATGTGCTACCACAGGGA

TrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuGluProPheArg
TGGAAAGGATCACCAGCAATATTCCAGAGTAGCATGACAAAAATCTTAGAACCCTTTAGA
                2600
ThrLysAsnProGluIleValIleTyrGlnTyrMetAspAspLeuTyrValGlySerAsp
ACAAAAAATCCAGAAATAGTCATATACCAATACATGGATGATTTGTATGTAGGGTCTGAT
                                                        2700
LeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGluHisLeuLeuLysTrp
TTAGAAATAGGACAACATAGAACAAAAATAGAGGAACTAAGAGAACATCTATTGAAATGG

GlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyr
GGATTTACCACACCAGACAAAAAGCATCAGAAAGAACCCCCATTTCTTTGGATGGGGTAT
                                        2800
GluLeuHisProAspLysTrpThrValGlnProIleGlnLeuProAspLysGluSerTrp
GAACTCCACCCTGACAAATGGACAGTGCAGCCTATACAACTGCCAGACAAGGAAAGCTGG

ThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIleTyrPro
ACTGTCAATGATATACAGAAATTGGTGGGAAAACTAAATTGGGCAAGTCAGATTTATCCA
                2900
GlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyAlaLysAlaLeuThrAspIle
GGAATTAAAGTAAAGCAATTATGTAAACTCCTTAGGGGAGCAAAAGCACTAACAGACATA
                                                        3000
ValProLeuThrAlaGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGlu
GTACCATTAACTGCAGAGGCAGAATTAGAATTGGCAGAGAACAGGGAAATTCTAAAAGAA
```

FIG. 7C

```
ProValHisGlyValTyrTyrAspProSerLysAspLeuIleAlaGluIleGlnLysGln
CCAGTGCATGGGGTATATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAG
                                             3100
GlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluGlnTyrLysAsnLeuLysThrGly
GGGCAAGGTCAATGGACATATCAAATATACCAAGAGCAATATAAAAATCTGAAAACAGGG

LysTyrAlaArgIleLysSerAlaHisThrAsnAspValLysGlnLeuThrGluAlaVal
AAGTATGCAAGAATAAAGTCTGCCCACACTAATGATGTAAAACAATTAACAGAAGCAGTG
               3200
GlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThrProLysPheArgLeuPro
CAAAAGATAGCCCAAGAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAGACTACCC
                                                        3300
IleGlnLysGluThrTrpGluAlaTrpTrpThrGluTyrTrpGlnAlaThrTrpIlePro
ATACAAAAAGAAACATGGGAGGCATGGTGGACAGAATATTGGCAAGCCACCTGGATCCCT

GluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluThrGlu
GAATGGGAGTTTGTCAATACTCCTCCCCTAGTAAAACTATGGTACCAGTTAGAAACAGAA
                                             3400
ProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysLys
CCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGAGAAACTAAAAAG

GlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSerLeuThrGluThr
GGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAGGTTGTCTCCTTAACTGAAACA
               3500
ThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspSerGlySerGlu
ACAAATCAGAAGACTGAATTACAAGCAATCCACTTAGCTTTACAGGATTCAGGATCAGAA
                                                        3600
ValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLys
GTAAACATAGTAACAGACTCACAGTATGCATTAGGGATTATTCAAGCACAACCAGATAAA

SerGluSerGluIleValAsnGlnIleIleGluGlnLeuIleGlnLysAspLysValTyr
AGTGAATCAGAGATTGTTAATCAAATAATAGAGCAATTAATACAGAAGGACAAGGTCTAC
                                             3700
LeuSerTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnValAspLysLeuVal
CTGTCATGGGTACCAGCACACAAAGGGATTGGAGGAAATGAACAAGTAGATAAATTAGTC

SerSerGlyIleArgLysValLeuPheLeuAspGlyIleAspLysAlaGlnGluGluHis
AGCAGTGGAATCAGAAAGGTACTATTTTTAGATGGGATAGATAAGGCTCAAGAAGAACAT
               3800
GluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeuProProIleVal
GAAAAATATCACAGCAATTGGAGAGCAATGGCTAGTGACTTTAATCTACCACCTATAGTA
                                                        3900
AlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGluAlaMetHisGly
GCGAAGGAAATAGTAGCCAGCTGTGATAAATGTCAACTAAAAGGGGAAGCCATGCATGGA

GlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeuGluGlyLysIle
CAAGTAGACTGTAGTCCAGGGATATGGCAATTAGATTGCACACATCTAGAAGGAAAAATA
                                             4000
IleIleValAlaValHisValAlaSerGlyTyrIleGluAlaGluValIleProAlaGlu
ATCATAGTAGCAGTCCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATCCCAGCAGAA

ThrGlyGlnGluThrAlaTyrPheIleLeuLysLeuAlaGlyArgTrpProValLysVal
ACAGGACAGGAGACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTAAAAGTA
               4100
```

FIG. 7D

ValHisThrAspAsnGlySerAsnPheThrSerAlaAlaValLysAlaAlaCysTrpTrp
GTACACACAGACAATGGCAGCAATTTCACCAGTGCTGCAGTTAAAGCAGCCTGTTGGTGG
4200
AlaAsnIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGlnGlyValValGlu
GCAAATATCAAACAGGAATTTGGAATTCCCTACAACCCCCAAAGTCAAGGAGTAGTGGAA

SerMetAsnLysGluLeuLysLysIleIleGlyGlnValArgGluGlnAlaGluHisLeu
TCTATGAATAAGGAATTAAAGAAAATCATAGGGCAGGTAAGAGAGCAAGCTGAACACCTT
4300
LysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLysGlyGlyIleGly
AAGACAGCAGTACAAATGGCAGTGTTCATTCACAATTTTAAAAGAAAAGGGGGGATTGGG

GlyTyrSerAlaGlyGluArgIleIleAspMetIleAlaThrAspIleGlnThrLysGlu
GGGTACAGTGCAGGGGAAAGAATAATAGACATGATAGCAACAGACATACAAACTAAAGAA
4400
LeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArgAspAsnArgAsp
TTACAAAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAGAGAC
4500
ProIleTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAlaValValIleGln
CCAATTTGGAAAGGACCAGCAAAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAG
→Q
AspAsnSerAspIleLysValValProArgArgLysAlaLysIleIleArgAspTyrGly
MetGlu
GACAATAGTGATATAAAGGTAGTACCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGA
4600 POL←
LysGlnMetAlaGlyAspAspCysValAlaGlyGlyGlnAspGluAsp
AsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIleArgThrTrpHis
AAACAGATGGCAGGTGATGATTGTGTGGCAGGTGGACAGGATGAGGATTAGAACATGGCA

SerLeuValLysHisHisMetTyrValSerLysLysAlaLysAsnTrpPheTyrArgHis
CAGTTTAGTAAAACATCATATGTATGTCTCAAAGAAAGCTAAAAATTGGTTTTATAGACA
4700
HisTyrGluSerArgHisProLysValSerSerGluValHisIleProLeuGlyAspAla
TCACTATGAAAGCAGGCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGGGATGC
4800
ArgLeuValValArgThrTyrTrpGlyLeuGlnThrGlyGluLysAspTrpHisLeuGly
TAGATTAGTAGTAAGAACATATTGGGGTCTGCAAACAGGAGAAAAAGACTGGCACTTGGG

HisGlyValSerIleGluTrpArgGlnLysArgTyrSerThrGlnLeuAspProAspLeu
TCATGGGGTCTCCATAGAATGGAGGCAGAAAAGATATAGCACACAACTAGATCCTGACCT
4900
AlaAspGlnLeuIleHisLeuTyrTyrPheAspCysPheSerGluSerAlaIleArgGln
AGCAGACCAACTGATTCATCTGTACTATTTTGATTGTTTTTCAGAATCTGCCATAAGACA

AlaIleLeuGlyHisIleValSerProArgCysAspTyrGlnAlaGlyHisAsnLysVal
AGCCATATTAGGACATATAGTTAGTCCTAGGTGTGATTATCAAGCAGGACATAACAAGGT
5000
GlySerLeuGlnTyrLeuAlaLeuThrAlaLeuIleAlaProLysLysThrArgProPro
AGGATCTTTACAGTATTTGGCACTAACAGCATTAATAGCACCAAAAAAGACAAGGCCACC
→R 5100
MetGluGlnAlaProAlaAspGlnGly
LeuProSerValArgLysLeuThrGluAspArgTrpAsnLysProGlnGlnThrLysGly
TTTGCCTAGTGTTAGGAAGCTAACAGAAGATAGATGGAACAAGCCCCAGCAGACCAAGGG

FIG. 7E

```
                                        Q←
ProGlnArgGluProHisAsnGluTrpThrLeuGluLeuLeuGluGluLeuLysGlnGlu
 HisArgGlySerHisThrMetAsnGlyHis
CCACAGAGGGAGCCACACAATGAATGGACATTAGAACTTTTAGAGGAGCTTAAGCAAGAA
                                          5200
AlaValArgHisPheProArgIleTrpLeuHisSerLeuGlyGlnHisIleTyrGluThr
GCTGTCAGACACTTTCCTAGGATATGGCTCCATAGTTTAGGACAACATATCTATGAAACT

TyrGlyAspThrTrpGluGlyValGluAlaIleIleArgSerLeuGlnGlnLeuLeuPhe
TATGGGGATACCTGGGAAGGAGTTGAAGCTATAATAAGAAGTCTGCAACAACTGCTGTTT
              5300
IleHisPheArgIleGlyCysGlnHisSerArgIleGlyIleThrArgGlnArgArgAla
ATTCATTTCAGAATTGGGTGTCAACATAGCAGAATAGGCATTACTCGACAGAGAAGAGCA
    →S         R←                                       5400
ArgAsnGlySerSerArgSer
    MetAspProValAspProAsnLeuGluProTrpAsnHisProGlySerGlnProArg
AGAAATGGATCCAGTAGATCCTAACTTAGAGCCCTGGAACCATCCAGGGAGTCAGCCTAG

 ThrProCysAsnLysCysTyrCysLysLysCysCysTyrHisCysGlnMetCysPheIle
GACGCCTTGTAATAAGTGTTATTGTAAAAAGTGCTGCTATCATTGCCAAATGTGCTTCAT
                                          5500
 ThrLysGlyLeuGlyIleSerTyrGlyArgLysLysArgArgGlnArgArgArgProPro
AACGAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCC
                                          S←
 GlnGlyAsnGlnAlaHisGlnAspProLeuProGluGln
TCAGGGCAATCAGGCTCATCAAGATCCTCTACCAGAGCAGTAAGTAGTATATGTAATACA
              5600
ACCTTTAGTGATATTAGCAATAGTAGCATTAGTAGTAACGCTAATAATAGCAATAGTTGT
                                                          5700
GTGGACCATAGTATTTATAGAAATTAGGAAAATAAGAAGACAAAGGAAAATAGACAGGTT
                                        →ENV
                                        MetArgValArgGluIleGlnArg
GATTGATAGAATAAGAGAAAGAGCAGAAGATAGTGGCAATGAGAGTGAGGGAGATACAGA
                                          5800
 AsnTyrGlnAsnTrpTrpArgTrpGlyMetMetLeuLeuGlyMetLeuMetThrCysSer
GGAATTATCAAAACTGGTGGAGATGGGGCATGATGCTCCTTGGGATGTTGATGACCTGTA

 IleAlaGluAspLeuTrpValThrValTyrTyrGlyValProValTrpLysGluAlaThr
GTATTGCAGAAGATTTGTGGGTTACAGTTTATTATGGGGTACCTGTGTGGAAAGAAGCAA
              5900
 ThrThrLeuPheCysAlaSerAspAlaLysSerTyrGluThrGluValHisAsnIleTrp
CCACTACTCTATTTTGTGCATCAGATGCTAAATCATATGAAACAGAAGTACATAACATCT
                                                          6000
 AlaThrHisAlaCysValProThrAspProAsnProGlnGluIleGluLeuGluAsnVal
GGGCTACACATGCCTGTGTACCCACGGACCCCAACCCACAAGAAATAGAACTGGAAAATG

 ThrGluGlyPheAsnMetTrpLysAsnAsnMetValGluGlnMetHisGluAspIleIle
TCACAGAAGGGTTTAACATGTGGAAAAATAACATGGTGGAGCAGATGCATGAGGATATAA
                                          6100
```

FIG. 7F

SerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrProLeuCysValThrLeu
TCAGTTTATGGGATCAAAGCCTAAAACCATGTGTAAAGCTAACCCCACTCTGTGTCACTT

AsnCysThrAsnValAsnGlyThrAlaValAsnGlyThrAsnAlaGlySerAsnArgThr
TAAACTGCACTAATGTGAATGGGACTGCTGTGAATGGGACTAATGCTGGGAGTAATAGGA
6200

AsnAlaGluLeuLysMetGluIleGlyGluValLysAsnCysSerPheAsnIleThrPro
CTAATGCAGAATTGAAAATGGAAATTGGAGAAGTGAAAAACTGCTCTTTCAATATAACCC
6300

ValGlySerAspLysArgGlnGluTyrAlaThrPheTyrAsnLeuAspLeuValGlnIle
CAGTAGGAAGTGATAAAAGGCAAGAATATGCAACTTTTTATAACCTTGATCTAGTACAAA

AspAspSerAspAsnSerSerTyrArgLeuIleAsnCysAsnThrSerValIleThrGln
TAGATGATAGTGATAATAGTAGTTATAGGCTAATAAATTGTAATACCTCAGTAATTACAC
6400

AlaCysProLysValThrPheAspProIleProIleHisTyrCysAlaProAlaGlyPhe
AGGCTTGTCCAAAGGTAACCTTTGATCCAATTCCCATACATTATTGTGCCCCAGCTGGTT

AlaIleLeuLysCysAsnAspLysLysPheAsnGlyThrGluIleCysLysAsnValSer
TTGCAATTCTAAAGTGTAATGATAAGAAGTTCAATGGAACGGAAATATGTAAAAATGTCA
6500

ThrValGlnCysThrHisGlyIleLysProValValSerThrGlnLeuLeuLeuAsnGly
GTACAGTACAATGTACACATGGAATTAAGCCAGTGGTGTCAACTCAACTGCTGTTAAATG
6600

SerLeuAlaGluGluGluIleMetIleArgSerGluAsnLeuThrAspAsnThrLysAsn
GCAGTCTAGCAGAAGAAGAGATAATGATTAGATCTGAAAATCTCACAGACAATACTAAAA

IleIleValGlnLeuAsnGluThrValThrIleAsnCysThrArgProGlyAsnAsnThr
ACATAATAGTACAGCTTAATGAAACTGTAACAATTAATTGTACAAGGCCTGGAAACAATA
6700

ArgArgGlyIleHisPheGlyProGlyGlnAlaLeuTyrThrThrGlyIleValGlyAsp
CAAGAAGAGGGATACATTTCGGCCCAGGGCAAGCACTCTATACAACAGGGATAGTAGGAG

IleArgArgAlaTyrCysThrIleAsnGluThrGluTrpAspLysThrLeuGlnGlnVal
ATATAAGAAGAGCATATTGTACTATTAATGAAACAGAATGGGATAAAACTTTACAACAGG
6800

AlaValLysLeuGlySerLeuLeuAsnLysThrLysIleIlePheAsnSerSerSerGly
TAGCTGTAAAACTAGGAAGCCTTCTTAACAAAACAAAAATAATTTTTAATTCATCCTCAG
6900

GlyAspProGluIleThrThrHisSerPheAsnCysArgGlyGluPhePheTyrCysAsn
GAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTAGAGGGGAATTTTTCTACTGTA

ThrSerLysLeuPheAsnSerThrTrpGlnAsnAsnGlyAlaArgLeuSerAsnSerThr
ATACATCAAAACTGTTTAATAGTACATGGCAGAATAATGGTGCAAGACTAAGTAATAGCA
7000

GluSerThrGlySerIleThrLeuProCysArgIleLysGlnIleIleAsnMetTrpGln
CAGAGTCAACTGGTAGTATCACACTCCCATGCAGAATAAAACAAATTATAAATATGTGGC

LysThrGlyLysAlaMetTyrAlaProProIleAlaGlyValIleAsnCysLeuSerAsn
AGAAAACAGGAAAAGCTATGTATGCCCCTCCCATCGCAGGAGTCATCAACTGTTTATCAA
7100

IleThrGlyLeuIleLeuThrArgAspGlyGlyAsnSerSerAspAsnSerAspAsnGlu
ATATTACAGGGCTGATATTAACAAGAGATGGTGGAAATAGTAGTGACAATAGTGACAATG
7200

FIG. 7G

ThrLeuArgProGlyGlyGlyAspMetArgAspAsnTrpIleSerGluLeuTyrLysTyr
AGACCTTAAGACCTGGAGGAGGAGATATGAGGGACAATTGGATAAGTGAATTATATAAAT

LysValValArgIleGluProLeuGlyValAlaProThrLysAlaLysArgArgValVal
ATAAAGTAGTAAGAATTGAACCCCTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGG
7300

GluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeuGlyPheLeuGlyAlaAla
TGGAAAGAGAAAAAAGAGCAATAGGACTAGGAGCCATGTTCCTTGGGTTCTTGGGAGCAG

GlySerThrMetGlyAlaAlaSerLeuThrLeuThrValGlnAlaArgGlnLeuLeuSer
CAGGAAGCACGATGGGCGCAGCGTCACTAACGCTGACGGTACAGGCCAGACAGTTACTGT
7400

GlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGlnHisLeuLeu
CTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAGGCGCAACAGCATCTGT
7500

GlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaValGluArgTyr
TGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT

LeuGlnAspGlnArgLeuLeuGlyMetTrpGlyCysSerGlyLysHisIleCysThrThr
ACCTACAGGATCAACGGCTCCTAGGAATGTGGGGTTGCTCTGGAAAACACATTTGCACCA
7600

PheValProTrpAsnSerSerTrpSerAsnArgSerLeuAspAspIleTrpAsnAsnMet
CATTTGTGCCTTGGAACTCTAGTTGGAGTAATAGATCTCTAGATGACATTTGGAATAATA

ThrTrpMetGlnTrpGluLysGluIleSerAsnTyrThrGlyIleIleTyrAsnLeuIle
TGACCTGGATGCAGTGGGAAAAAGAAATTAGCAATTACACAGGCATAATATACAACTTAA
7700

GluGluSerGlnIleGlnGlnGluLysAsnGluLysGluLeuLeuGluLeuAspLysTrp
TTGAAGAATCGCAAATCCAGCAAGAAAAGAATGAAAAGGAATTATTGGAATTGGACAAGT
7800

AlaSerLeuTrpAsnTrpPheSerIleSerLysTrpLeuTrpTyrIleArgIlePheIle
GGGCAAGTTTGTGGAATTGGTTTAGCATATCAAAATGGCTGTGGTATATAAGAATATTCA

IleValValGlyGlyLeuIleGlyLeuArgIleIlePheAlaValLeuSerLeuValAsn
TAATAGTAGTAGGAGGCTTAATAGGTTTAAGAATAATTTTTGCTGTGCTTTCTTTAGTAA
7900

ArgValArgGlnGlyTyrSerProLeuSerLeuGlnThrLeuLeuProThrProArgGly
ATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTGCAGACCCTCCTCCCAACACCGAGGG

ProProAspArgProGluGlyIleGluGluGluGlyGlyGluGlnGlyArgGlyArgSer
GACCACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGCAAGGCAGAGGCAGAT
8000

IleArgLeuValAsnGlyPheSerAlaLeuIleTrpAspAspLeuArgAsnLeuCysLeu
CAATTCGATTGGTGAACGGATTCTCAGCACTTATCTGGGACGACCTGAGGAACCTGTGCC
8100

PheSerTyrHisArgLeuArgAspLeuLeuLeuIleAlaThrArgIleValGluLeuLeu
TCTTCAGTTACCACCGCTTGAGAGACTTACTCTTAATTGCAACGAGGATTGTGGAACTTC

GlyArgArgGlyTrpGluAlaLeuLysTyrLeuTrpAsnLeuLeuGlnTyrTrpGlyGln
TGGGACGCAGGGGGTGGGAAGCCCTCAAATATCTGTGGAATCTCCTGCAATATTGGGGTC
8200

FIG. 7H

```
GluLeuLysAsnSerAlaIleSerLeuLeuAsnThrThrAlaIleAlaValAlaGluCys
AGGAACTGAAGAATAGTGCTATTAGCTTGCTTAATACCACAGCAATAGCAGTAGCTGAAT

ThrAspArgValIleGluIleGlyGlnArgPheGlyArgAlaIleLeuHisIleProArg
GCACAGATAGGGTTATAGAAATAGGACAAAGATTTGGTAGAGCTATTCTCCACATACCTA
            8300                         ->F
                             EW<-       MetGlyGlyLysTrpSerLys
ArgIleArgGlnGlyPheGluArgAlaLeuLeu
GAAGAATTAGACAGGGCTTCGAAAGGGCTTTGCTATAACATGGGTGGCAAGTGGTCAAAA
                                                        8400
SerSerIleValGlyTrpProLysIleArgGluArgIleArgArgThrProProThrGlu
AGTAGCATAGTAGGATGGCCTAAGATTAGGGAAAGAATAAGACGAACTCCCCCAACAGAA

ThrGlyValGlyAlaValSerGlnAspAlaValSerGlnAspLeuAspLysCysGlyAla
ACAGGAGTAGGAGCAGTATCTCAAGATGCAGTATCTCAAGATTTAGATAAATGTGGAGCA
                                    8500
AlaAlaSerSerSerProAlaAlaAsnAsnAlaSerCysGluProProGluGluGluGlu
GCCGCAAGCAGCAGTCCAGCAGCTAATAATGCTAGTTGTGAACCACCAGAAGAAGAGGAG

GluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLysGlyAla
GAGGTAGGCTTTCCAGTCCGTCCTCAGGTACCTTTAAGACCAATGACTTATAAAGGAGCT
            8600                      ->U3
PheAspLeuSerHisPheLeuLysGluLysGlyGlyLeuAspGlyLeuValTrpSerPro
TTTGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGATGGGTTAGTTTGGTCCCCA
                                                        8700
LysArgGlnGluIleLeuAspLeuTrpValTyrHisThrGlnGlyTyrPheProAspTrp
AAAAGACAAGAAATCCTTGATCTGTGGGTCTACCACACACAAGGCTACTTCCCTGATTGG

GlnAsnTyrThrProGlyProGlyIleArgPheProLeuThrPheGlyTrpCysPheLys
CAGAATTACACACCAGGGCCAGGGATTAGATTCCCACTGACCTTCGGATGGTGCTTTAAG
                                    8800
LeuValProMetSerProGluGluValGluGluAlaAsnGluGlyGluAsnAsnCysLeu
TTAGTACCAATGAGTCCAGAGGAAGTAGAGGAGGCCAATGAAGGAGAGAACAACTGTCTG

LeuHisProIleSerGlnHisGlyMetGluAspAlaGluArgGluValLeuLysTrpLys
TTACACCCTATTAGCCAACATGGAATGGAGGACGCAGAAAGAGAAGTGCTAAAATGGAAG
            8900
PheAspSerSerLeuAlaLeuArgHisArgAlaArgGluGlnHisProGluTyrTyrLys
TTTGACAGCAGCCTAGCACTAAGACACAGAGCCAGAGAACAACATCCGGAGTACTACAAA
 F<-                                                    9000
AspCys
GACTGCTGACACAGAAGTTGCTGACAGGGGACTTTCCGCTGGGGACTTTCCAGGGGAGGC

GTAACTTGGGCGGGACCGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGCTGCTT
          U3<->R                    9100
TTCGCCTGTACTGGGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGC

AAGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAA
            9200
```

FIG. 7I

FIG. 1A

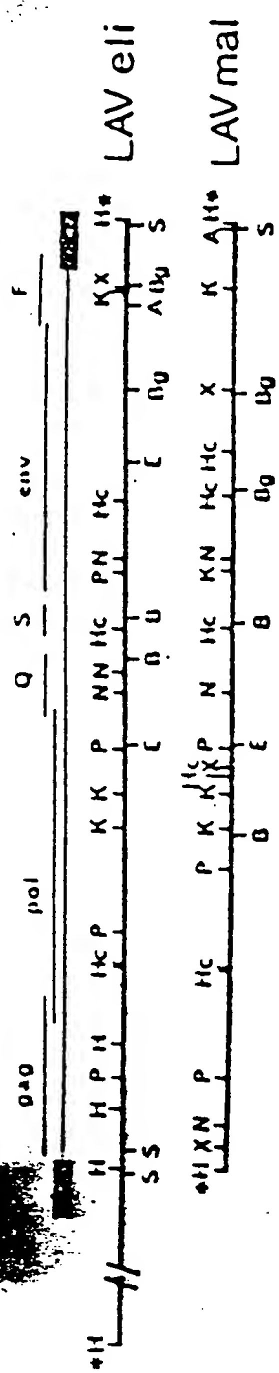

LAV eli
LAV mal
gag
pol
env
Q
S
F

FIG. 1B

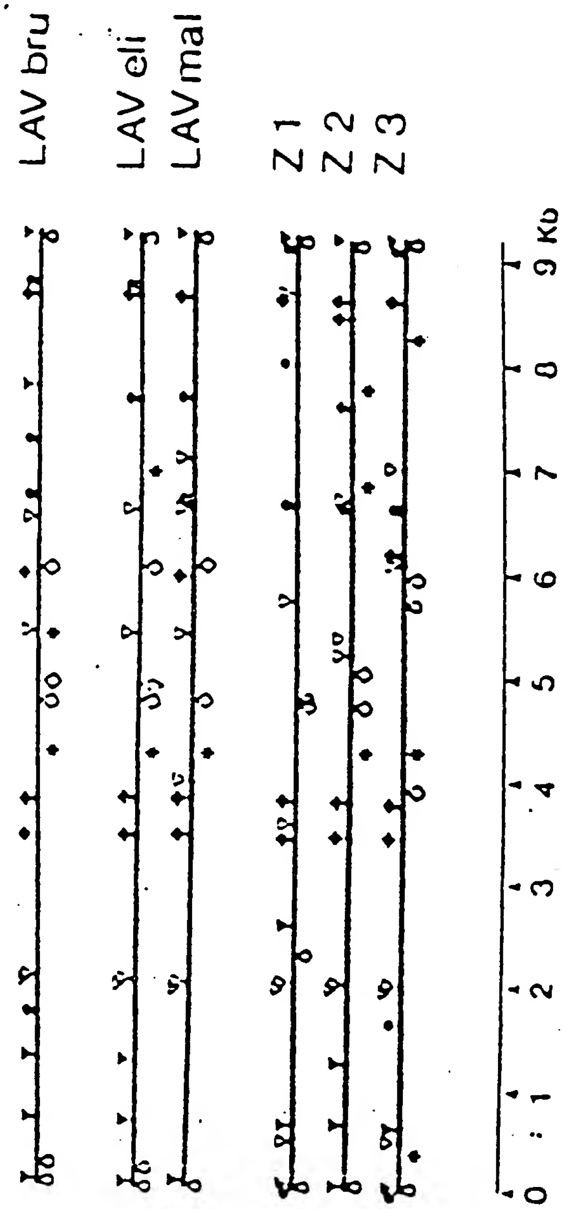
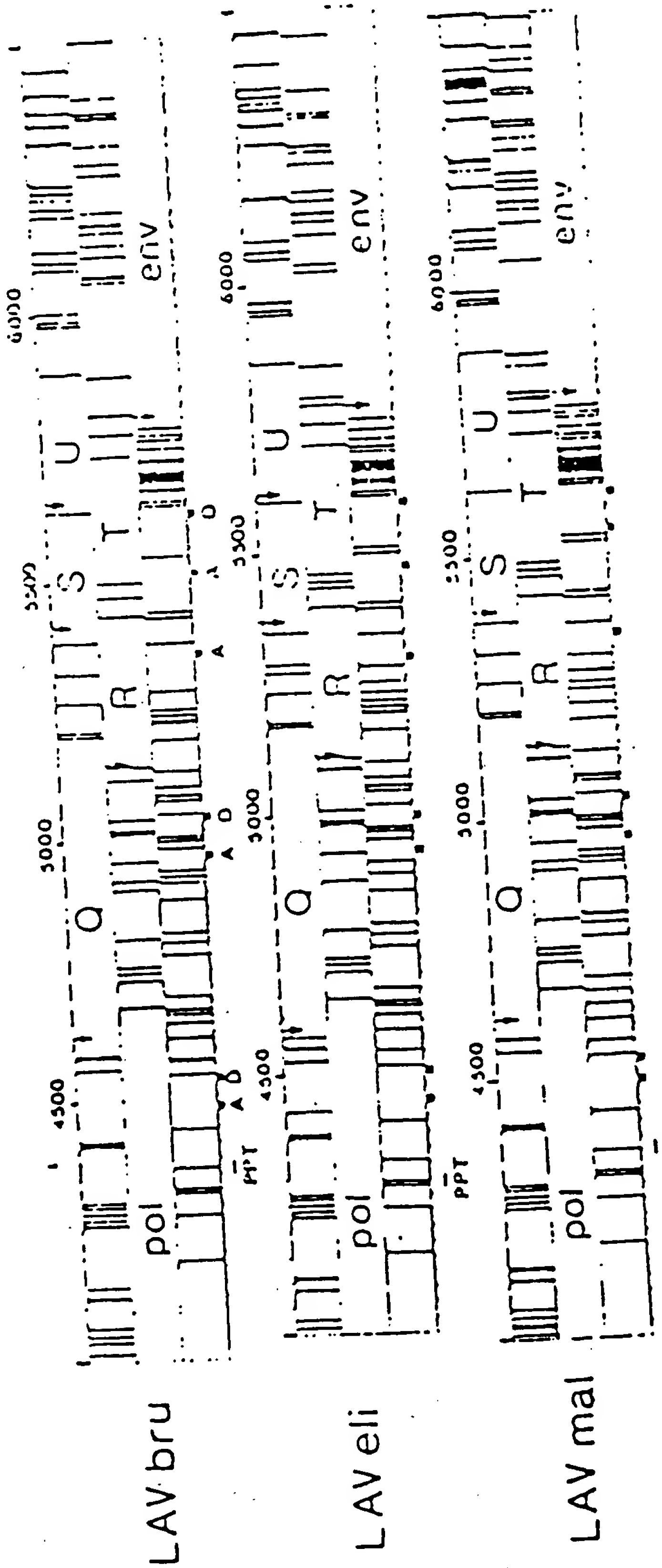

LAV bru
LAV eli
LAV mal
Z 1
Z 2
Z 3
0
1
2
3
4
5
6
7
8
9 Kb

FIG. 2



Coll
66

GAG

```
                  10         20         30         40         50         60         70         80
LAV BRU   MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                      K
LAV MAL               K    A          R     L          L         C    Q   ME  ST K      IK
LAV ELI               K    K          R               Y L             K   I    AI    T
                                                                         |p25
                  90        100        110        120        130        140        150        160
LAV BRU   TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGH SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                   DV         E                ----AAG  N               L
LAV MAL                 DV         .    I    NQ T   AQQAAA KN    S           A    I
LAV ELI               K G DV       E M              ------   N N             L

                 170        180        190        200        210        220        230        240
LAV BRU   WVKVVEEKAF SPEVIPMFSA LSEGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDR VHPVHAGPIA PGQMREPRGS
ARV 2
LAV MAL      I                           M    I           D         D                P
LAV ELI      I                                                                L

                 250        260        270        280        290        300        310        320
LAV BRU   DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                        D
LAV MAL                   S         D                    V                        F      T
LAV ELI              A    S                  V           V                                   D
                                                                                  |p13
                 330        340        350        360        370        380        390        400
LAV BRU   NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                               P-   N              T
LAV MAL                           G                     S         A    T  A       KG - KI
LAV ELI                           Q                     S         A    V  T A     KGP    I

                 410        420        430        440        450        460        470        480
LAV BRU   NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPEE
ARV 2             K          R  R                                             ---- --------
LAV MAL         L                                          N                  ---- ---------A
LAV ELI           K          R      L                R     N                  ---- ---------A

                 490        500        510
LAV BRU   SFRSGVETTT PSQKQEPIDK ELYPLTSLKS LFGNDPSSQ
ARV 2       F  E K
LAV MAL     GF  E IK-     QK        A  K      QL
LAV ELI     GF  E I -     QK           K       L
```

FIG. 3A

FIG. 3B

Central region :

Q

```
                 10         20         30         40         50         60         70         80
LAV BRU  HENRWQVHIV WQVDRHRIRT WKSLVKHHHY VSCKARGWFY KHHYESPHPR ISSEVHIPLG DARLVITTYW GLHTGERDWH
ARV 2                                     I K  K           T    V            K               E
LAV MAL                         H           K  KH          R  K V               VR      Q   K
LAV ELI                      K              K  HK             K            E     K           E

                 90        100        110        120        130        140        150        160
LAV BRU  LCQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK
ARV 2         A       K        G        H       E    KH I  YR                                T
LAV MAL    H        Q      L   D                E     Q I                     D       T   A  TR
LAV ELI              R         G       H        E       I  D                          T   A  Q

                170        180        190
LAV BRU  PPLPSVTKLT EDRWNKPQKT KGHRGSHTMN GH
ARV 2          K
LAV MAL        R            Q
LAV ELI        R            Q   R
```

R

```
                 10         20         30         40         50         60         70         80
LAV BRU  HEQAPEDQGP QREPHHEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                   Y             R         P    S   Y                                  Q
LAV MAL       A                       Q              S              E        S              Q
LAV ELI       A         Y   A         S              S              V                       Q

                 90
LAV BRU  IGVTQQRRAR -NGASRS
ARV 2      II       R
LAV MAL    I R      -  S
LAV ELI    IIR      -  S
```

S (tat)

```
                 10         20         30         40         50         60         70
LAV BRU  HEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2          H            R    HH           YA   R  G                 A  D     A
LAV MAL   D    N     N      R  P HK         Y   H  I   G                     H A  DP P E
LAV ELI   D    N     N      R  P HK H       Y  P   LH  G                G    G A   PIP
```

POL

```
                    10         20         30         40         50         60         70         80
LAV BRU    FFREDLAFLQ GKAREFSSEQ TRANSPTFSS EQTRANSPTR RELQVWGRDN NSLSEACADR QCTVSFNFPQ ITLWQRPLVT
ARV 2                                    --- ---------                  GE
LAV HAL        H   P        P            --- ---------S    R   C - KT   T  E    I   S           V
LAV ELI        H   P     C L PK          --- ---------S    R     -  P  KT  E                      A

                    90        100        110        120        130        140        150        160
LAV BRU    IKIGGQLKEA LLDTGADDTV LEENSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2       R                         N   K                         PV
LAV HAL    VRV                       IN   K                                K      I              H
LAV ELI                               N   K                         P      Q

                   170        180        190        200        210        220        230        240
LAV BRU    IGCTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV HAL                                R                  T   KD         L
LAV ELI                                                   T    D          R           I

                   250        260        270        280        290        300        310        320
LAV BRU    LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2                                                          K
LAV HAL      K
LAV ELI                                                                    S

                   330        340        350        360        370        380        390        400
LAV BRU    KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2                                                                             F
LAV HAL                         T K  E                                  E   K     F
LAV ELI                              EH                              K  E         F R

                   410        420        430        440        450        460        470        480
LAV BRU    LHPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                  H                             A     K
LAV HAL                Q  D E                              K         A    DIV     A
LAV ELI             S  K    E          H   ER

                   490        500        510        520        530        540        550        560
LAV BRU    VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARTRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2        E          V                                   H                    VS          I
LAV HAL                                       QY            IKS                   AQ              R
LAV ELI                           H                         H            A      R S          R    R
```

FIG. 3C

```
                570        580        590        600        610        620        630        640
LAV BRU  QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAASRETKLG KACYVTKRGR QKVVTLTDTT
ARV 2      I   A  H                                                 N             D        SIA
LAV HAL        A                                 T                  N   K         D        S  E
LAV ELI           A                                   I             N             D        P

                650        660        670        680        690        700        710        720
LAV BRU  HQKTELQAIH LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QLIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                     S
LAV HAL                    S                            I          Q D     S
LAV ELI           K

                730        740        750        760        770        780        790        800
LAV BRU  ACIRKVLFLD GIDKAQDEHE KYHSNWRAHA SDFNLPPVVA KEIVASCDKC QLKGEAHHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2             N       E                                                                   I
LAV HAL  S                E                      I                                            I
LAV ELI  Q                E       N

                810        820        830        840        850        860        870        880
LAV BRU  LVAVHVASGY IEAEVIPAET GQETAYFLLK LAGRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
LAV HAL  I                            I           VV            AA         N
LAV ELI                                           VV            AA

                890        900        910        920        930        940        950        960
LAV BRU  HHKELKKIIG QVRDQAEHLK TAVQHAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSKDP
ARV 2      N                                                                                KK
LAV HAL                E                                    I H                             H
LAV ELI                                      RR           I                  I

                970        980        990       1000       1010
LAV BRU  LWKGPAKLLW KCEGAVVIQD HSDIKVVPRR KAKIIRDYGK QHAGDDCVAS RQDED
ARV 2
LAV HAL  I                                                    G G
LAV ELI  I                     K           V
```

FIG. 3D

```
ENV                               SP                              OMP
                        10         20         30           40         50         60         70         80
LAV BRU        MRVK---EKY QMLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2           K  GTRRN            ---- - L    H                                 R
LAV MAL           RELQRH  NW        --- -H    H   T    IA  D                          S E         I
LAV ELI          ARGIEHHC  HW K     --- -I        T     ADH                           S E   A     I

                        90        100        110        120        130        140        150        160
LAV BRU        DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-GN ATNTNSSNTN SSSGEMMME-
ARV 2                   C          N     Q                          T N    - K           ---  ----KUKE I
LAV MAL              IE E      G          N                          T N  NVN T   V CTNACS  RTNA LK   I
LAV ELI              IA E                 N                          T N  S E--L RN CTNG NV TTLEKG----

                       170        180        190        200        210        220        230        240
LAV BRU        KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                      T    D I    N L RN  VV    AS T TNYTN R IN   R                        T
LAV MAL        -  V        TPVGSD R    -   T  N  LVQ   DSDN  ----S K IN                   T D
LAV ELI        ---N        VT VLKD K   QV   L  K    V     SST -NSTN K IN      A

                       250        260        270        280        290        300        310        320
LAV BRU        LKCNNKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2                     K             I                       D     N             E  A
LAV MAL            D K    EI  K             K                 IM    E   L   T N      ET  T         G    R
LAV ELI           RD K                                         I    E   L N   N   AN   E  K T   A  YQ    Q

                       330        340        350        360        370        380        390        400
LAV BRU        SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT HSFNCGGEFF
ARV 2            Y --        H  T RI  DI K          Q   N   E   VK           - V N              H      R
LAV MAL        G NF--     Q  LY  T I-V DI R  Y  T N ETE DK   Q  V V  GSLL- -   K  NS              T      R
LAV ELI        RTP  -- L Q SLY  TKS-RS IIG              Q SK   Q  V R  GTLL- -   I K  P              T

                       410        420        430        440        450        460        470        480
LAV BRU        YCNSTQLFNS TWFNSTWSTE GSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
ARV 2             T     N  -----RLN NTEG  K  N    I       I                  G  S                  T -V
LAV MAL           TSK      Q NGAKL-  -   S   STGS          I     KT          A  V  N  L      I     NSSD
LAV ELI           TSG      NI  A NNI TES NSTNTN      Q       I   K VAGR-   I     EAN   L               I --

                       490        500        510        520        530        540 TMP      550        560
LAV BRU        NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GARSMTLTVQ
ARV 2          T  DT  V                     I        I                        V  N                  V L
LAV MAL          SDN  TL            I        R                     E      I L-   H                  A L
LAV ELI          STN  T                      Q             R       E      I L-   H                    V
```

FIG. 3E

```
                   570        580        590        600        610        620        630        640
LAV BRU   ARQLLSGIVQ QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW NASWSNKSLE
ARV 2                                           V          R                  H    P     S    R  D
LAV HAL                                         V          Q    R    H        H    N     S    R  N
LAV ELI          H

                   650        660        670        680        690        700        710        720
LAV BRU   QIWNNMTWME WDREINNYTS LIHSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2     D  D    Q  E    D   N T YT L                          S
LAV HAL   D        Q  EK   S   G I YN          I      K          S  SK     R   IV     I    I
LAV ELI   E  Q         E   D   G  Y            T      K          S  Q              I    I

                   730        740        750        760        770        780        790        800
LAV BRU   VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PEGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                          R  V   -    D                V   D F        E          R        AA
LAV HAL       L             L  L      P                 QG G         FS           H             A
LAV ELI       L                L    A  -       T         G      V   L  FS                       I  AV

                   810        820        830        840        850        860        870
LAV BRU   RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2      T  I  N            S       I            W          T          A  R Y   L  H       L
LAV HAL                    L          G         I      T    [K]        IG RYG   L         F  A
LAV ELI                DI  L               R    S    FD  I             II  K    VLN           S

F
                   10         20         30         40         50         60         70         80
LAV BRU   .MGGKWSKSSV VGWPTVRERM R----RAEPA ADGVGAASR- ----DLEKHG AITSSNTAAT NAACAWLEAQ EE-EEVGFPV
ARV 2          R  H G   SAI       RAEP          V  - ----                      D             -
LAV HAL          I        KI   I  ---- TP  T  ET  V QD  AVSQ  D  C    AA   SP  N  S --- PP  E
LAV ELI          I        AI   I  ---- TH         V  -  ----                      S  D          SD

                   90         100        110        120        130        140        150        160
LAV BRU   TPQVPLRPMT YKAAVDLSHF LKEKGGLEGL IHSQRRQDIL DLWIYHTQGY FPDWQNYTPG PGVRYPLTFG WCYKLVPVEP
ARV 2     R               L I                   W      E                            I           F
LAV HAL   R             G F              D     VG  PK  E      V                    I  F        F    HS
LAV ELI   N             E L                    W  KK   E      V  N    I            I           E     D

                   170        180        190        200        210
LAV BRU   DKVEEANKGE NTSLLHPVSL HGHDDPEREV LEWRFDSRLA FHHVARELHP EYFKNC
ARV 2     E      E     H        H       E  A  K      V      K        H       Y  D
LAV HAL   EE     E     NC       I  Q    E  A         K  K   S     LR R   Q    Y  D
LAV ELI   QE    DTE    TN       ICQ     E      Q     K    N       E K     N    FY  - . :
```

FIG. 3F

A

LAVbru vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli Zaire	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal Zaire	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9

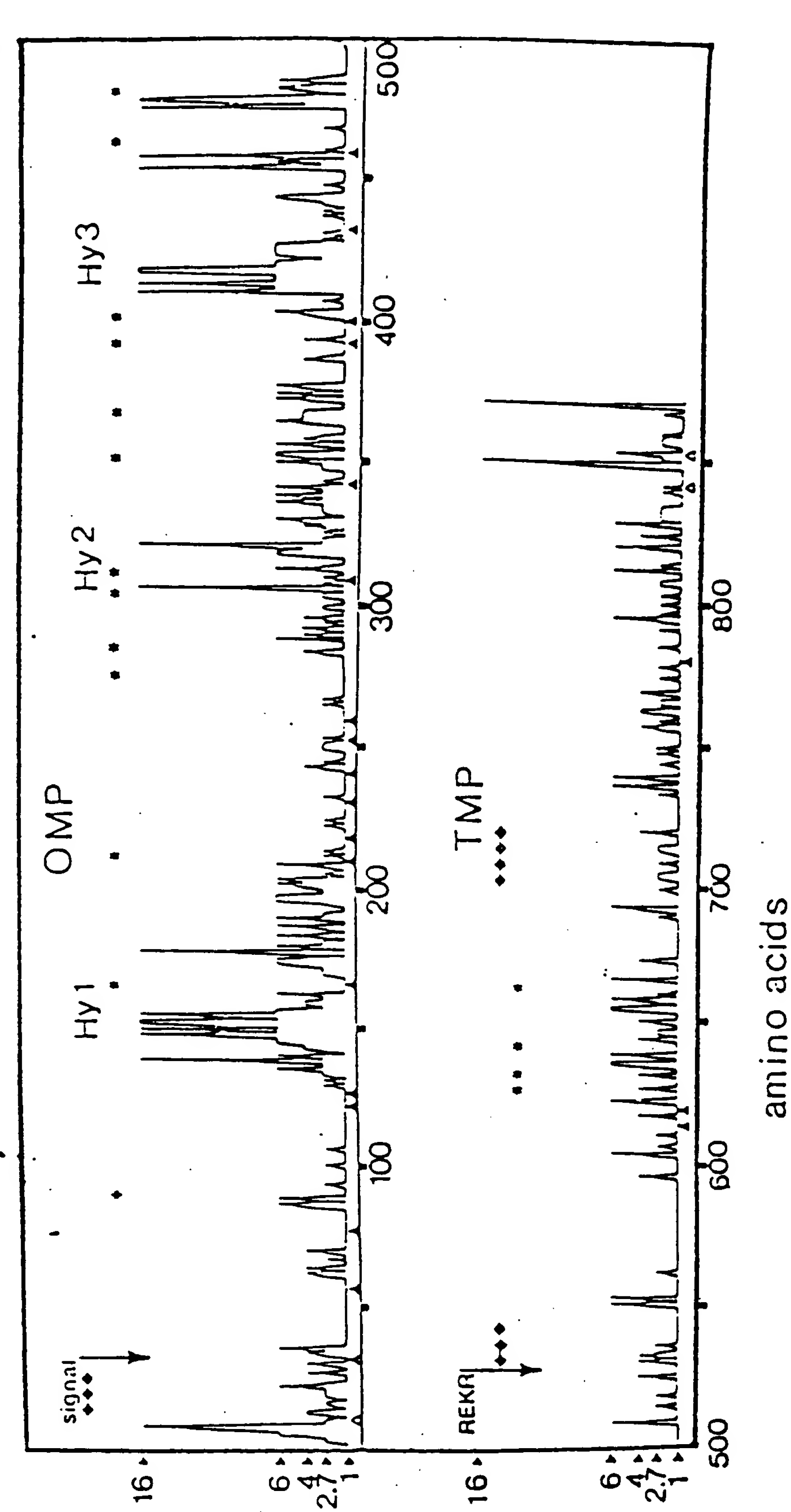
B

LAVeli vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4A

FIG. 4B

A L'AVbru vs.	orf F		central region: orf Q		orf R		orf S	
HTLV-3 USA	206 0/0	1.5	192 0/0	0	,	nd	80 0/0	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli Zaire	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal Zaire	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8
B LAVeli vs.								
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3



OMP
TMP
Hy 1
Hy 2
Hy3
signal
REKR
variability
amino acids
16
6
4
2.7
1
100
200
300
400
500
600
700
800

FIG. 5

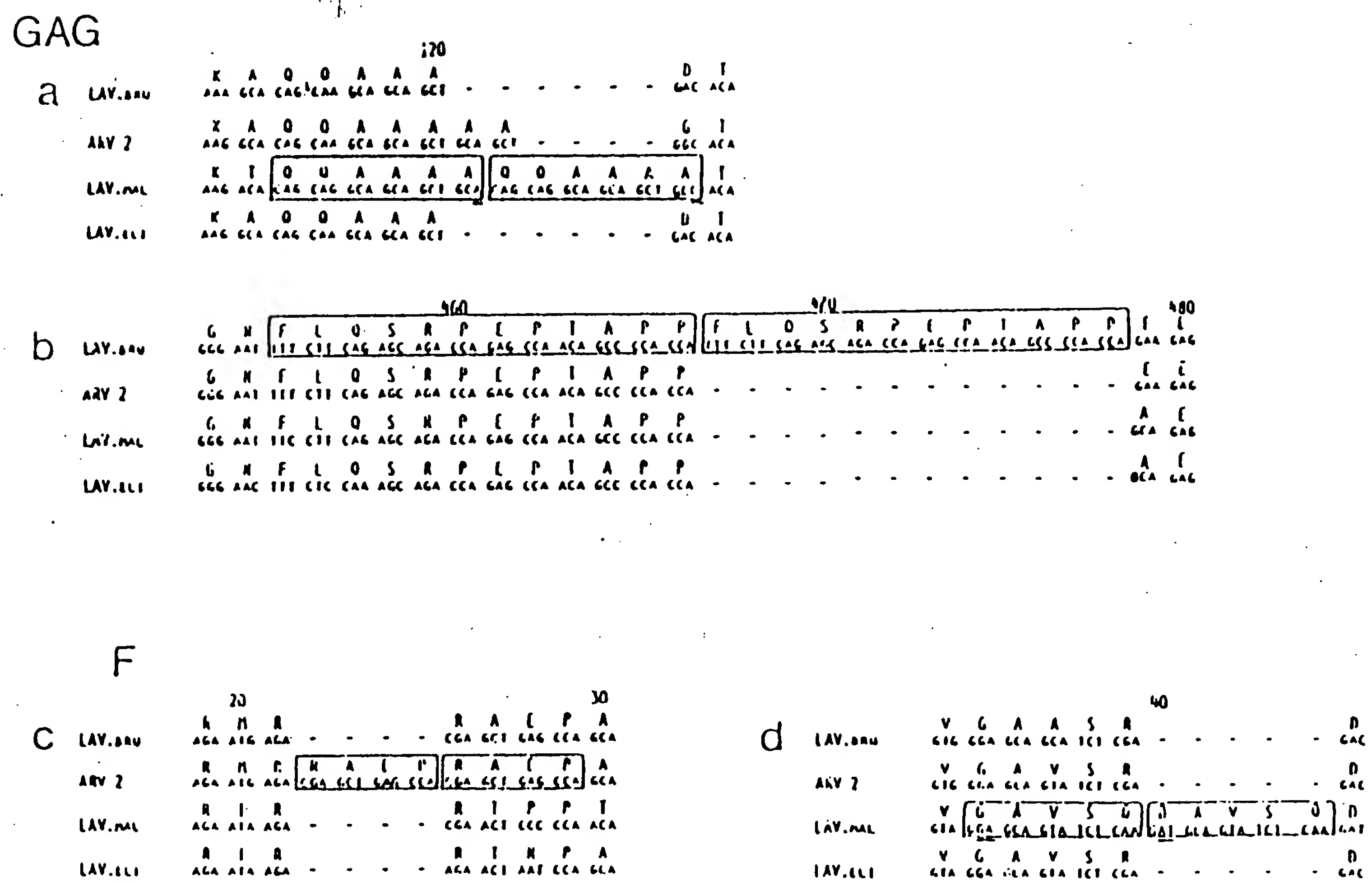


FIG. 6A

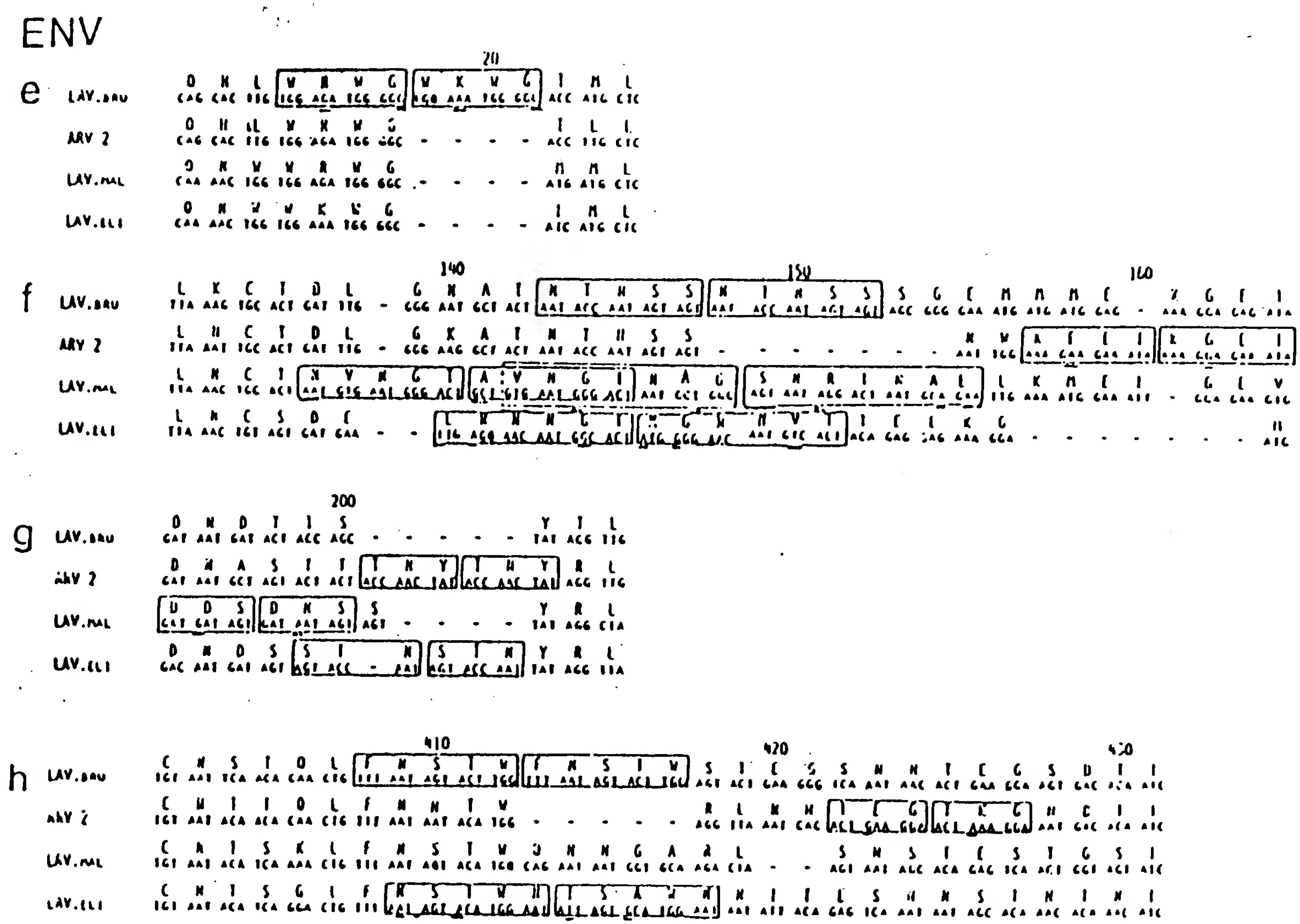

ENV
e
f
g
h
LAV.BRU
ARV 2
LAV.MAL
LAV.ELI
20
140
150
160
200
410
420
430

FIG. 6B

FIG. 7A

LAV.MAL

R

GGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGCAAGGAACCCACTG

R U5

CTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAAGCAGTGTGTGCCCATCTGTTGTGT

100 U5

GACTCTGGTAACTAGAGATCCCTCAGACCACTCTAGACGGTGTAAAAATCTCTAGCAGTG

GCGCCCGAACAGGGACTTTAAAGTGAAAGTAACAGGGACTCGAAAGCGGAAGTTCCAGAG

200

AAGTTCTCTCGACGCAGGACTCGGCTTGCTGAGGTGCACACAGCAAGAGGCGAGAGCGGC

300

GAG

MetGlyAlaArg

GACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAG

AlaSerValLeuSerGlyGlyLysLeuAspAlaTrpGluLysIleArgLeuArgProGly

AGCGTCAGTATTAAGCGGGGGAAAATTAGATGCATGGGAGAAAATTCGGTTAAGGCCAGG

400

GlyLysLysLysTyrArgLeuLysHisLeuValTrpAlaSerArgGluLeuGluArgPhe

GGGAAAGAAAAAATATAGACTGAAACATTTAGTATGGGCAAGCAGGGAGCTGGAAAGATT

AlaLeuAsnProGlyLeuLeuGluThrGlyGluGlyCysGlnGlnIleMetGluGlnLeu

CGCACTTAACCCTGGCCTTTTAGAAACAGGAGAAGGATGTCAACAAATAATGGAACAGCT

500

GlnSerThrLeuLysThrGlySerGluGluIleLysSerLeuTyrAsnThrValAlaThr

ACAATCAACTCTCAAGACAGGATCAGAAGAAATTAAATCATTATATAATACAGTAGCAAC

600

LeuTyrCysValHisGlnArgIleAspValLysAspThrLysGluAlaLeuAspLysIle

CCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACCAAGGAAGCGCTAGATAAAAT

GluGluIleGlnAsnLysSerArgGlnLysThrGlnGlnAlaAlaAlaAlaGlnGlnAla

AGAGGAAATACAAAATAAGAGCAGGCAAAAGACACAGCAGGCAGCAGCTGCACAGCAGGC

700

AlaAlaAlaThrLysAsnSerSerSerValSerGlnAsnTyrProIleValGlnAsnAla

AGCAGCTGCCACAAAAAACAGCAGCAGTGTCAGTCAAAATTACCCCATAGTGCAAAATGC

GlnGlyGlnMetIleHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysVal

ACAAGGGCAAATGATACATCAGGCCATATCACCTAGGACTTTGAATGCATGGGTGAAAGT

800

IleGluGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeuSerGluGly

AATAGAAGAAAAAGGCTTTCAGCCCAGAAGTGATACCCATGTTCTCAGCATTATCAGAGGG

900

AlaThrProGlnAspLeuAsnMetMetLeuAsnIleValGlyGlyHisGlnAlaAlaMet

GGCCACCCCACAAGATTTAAATATGATGCTGAACATAGTTGGAGGACACCAGGCAGCTAT

GlnMetLeuLysAspThrIleAsnGluGluAlaAlaAspTrpAspArgValHisProVal

GCAAATGTTAAAAGATACCATCAATGAGGAAGCTGCAGACTGGGACAGGGTACATCCAGT

1000

HisAlaGlyProIleProProGlyGlnMetArgGluProArgGlySerAspIleAlaGly

ACATGCAGGGCCTATTCCCCCAGGCCAGATGAGAGAACCAAGAGGAAGTGACATAGCAGG

FIG. 7B

```
Thr[illegible]LeuGlnGluGlnIleGlyTrpMetThrSerAsnProProIleProVal
AACTA[illegible]TACCCTTCAAGAACAAATAGGATGGATGACAAGCAACCCACCTATCCCAGT
     .          1100         .          .          .          .
GlyAspIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSer
GGGAGACATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAATGTATAG
     .          .          .          .          .       1200
ProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAspTyrValAsp
CCCTGTCAGCATTTTGGACATAAGACAAGGGCCAAAGGAACCTTTTAGAGACTATGTAGA
     .          .          .          .          .          .
ArgPhePheLysThrLeuArgAlaGluGlnAlaThrGlnGluValLysAsnTrpMetThr
TAGGTTCTTTAAAACTCTCAGAGCTGAGCAAGCTACACAGGAGGTAAAAAATTGGATGAC
     .          .          .        1300         .          .
GluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGly
AGAAACCTTGCTGGTCCAAAATGCGAATCCAGACTGTAAGACCATTTTAAAAGCATTAGG
     .          .          .          .          .          .
ProGlyAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProSerHis
ACCAGGGGCTACATTAGAAGAAATGATGACAGCATGCCAGGGAGTGGGAGGACCCAGTCA
     .          1400         .          .          .          .
LysAlaArgValLeuAlaGluAlaMetSerGlnAlaThrAsnSerThrAlaAlaIleMet
TAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAACAAATTCAACTGCTGCCATAAT
     .          .          .          .          .       1500
MetGlnArgGlyAsnPheLysGlyGlnLysArgIleLysCysPheAsnCysGlyLysGlu
GATGCAGAGAGGTAATTTTAAGGGCCAGAAAAGAATTAAGTGTTTCAACTGTGGCAAAGA
     .          .          .          .          .          .
GlyHisLeuAlaArgAsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLys
AGGACACCTAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGAA
     .          .          .        1600     →POL   .          .
                                             PhePheArgGluAsnLeu
GluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrp
GGAAGGACACCAAATGAAAGACTGCACTGAGAGACAGGCTAATTTTTTAGGGAAAATTTG
     .          .          .          .          .          .
AlaPheProGlnGlyLysAlaArgGluPheProSerGluGlnThrArgAlaAsnSerPro
 ProSerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaPro
GCCTTCCCACAAGGGAAGGCCAGGGAATTTCCTTCAGAGCAGACCAGAGCCAACAGCCCC
     .          1700         .          .          .          .
ThrSerArgGluLeuArgValTrpGlyGlyAspLysThrLeuSerGluThrGlyAlaGlu
 ProAlaGluSerPheGlyPheGlyGluGluIleLysProSerGlnLysGlnGluGlnLys
ACCAGCAGAGAGCTTCGGGTTTGGGGAGGAGATAAAACCCTCTCAGAAACAGGAGCAGAA
     .          .          .          .          .       1800
ArgG[illegible]GlyIleValSerPheSerPheProGlnIleThrLeuTrpGlnArgProValVal
 As[illegible]GluLeuTyrProLeuAlaSerLeuLysSerLeuPheGlyAsnAspGlnLeuSer
AGA[illegible]GCAATTGTATCCTTTAGCTTCCCTCAAATCACTCTTTGGCAACGACCAGTTGTC
GAG←  .          .          .          .          .          .
ThrValArgValGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyAlaAspAspThr
 Gln
ACAGTAAGAGTAGGAGGACAGCTAAAAGAAGCTCTATTAGACACAGGAGCAGATGATACA
     .          .          .        1900         .          .
ValLeuGluGluIleAsnLeuProGlyLysTrpLysProLysMetIleGlyGlyIleGly
GTATTAGAAGAAATAAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGA
     .          .          .          .          .          .
GlyPheIleLysValArgGlnTyrAspGlnIleLeuIleGluIleCysGlyLysLysAla
GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGCT
     .          2000         .          .          .          .
```

FIG. 7C

```
IleGlyThrIleLeuValGlyProThrProValAsnIleIleGlyArgAsnMetLeuThr
ATAGGTACAATATTGGTAGGACCTACACCTGTCAACATAATTGGACGAAATATGTTGACT
                                                        2100
GlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValProValLysLeu
CAGATTGGTTGTACTTTAAATTTTCCAATTAGTCCTATTGAGACTGTACCAGTAAAATTA

LysProGlyMetAspGlyProArgValLysGlnTrpProLeuThrGluGluLysIleLys
AAGCCAGGGATGGATGGCCCAAGGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA
                                    2200
AlaLeuThrGluIleCysLysAspMetGluLysGluGlyLysIleLeuLysIleGlyPro
GCATTAACAGAAATTTGTAAAGATATGGAAAAGGAAGGAAAAATTTTAAAAATTGGGCCT

GluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSerThrLysTrpArg
GAAAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGCACTAAATGGAGA
            2300
LysLeuValAsnPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluValGlnLeu
AAATTAGTGAATTTCAGAGAGCTTAATAAAAGAACTCAAGATTTTTGGGAAGTTCAATTA
                                                        2400
GlyIleProHisProAlaGlyLeuLysLysLysLysSerValThrValLeuAspValGly
GGAATACCACATCCTGCTGGGTTGAAAAAGAAAAAATCAGTCACAGTATTGGATGTGGGG

AspAlaTyrPheSerValProLeuAspGluAspPheArgLysTyrThrAlaPheThrIle
GATGCATATTTTTCAGTCCCTTTAGATGAAGATTTCAGGAAGTATACTGCATTCACTATA
                                    2500
ProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnValLeuProGlnGly
CCCAGTATTAATAATGAGACACCAGGGATTAGATATCAGTACAATGTGCTACCACAGGGA

TrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuGluProPheArg
TGGAAAGGATCACCAGCAATATTCCAGAGTAGCATGACAAAAATCTTAGAACCCTTTAGA
            2600
ThrLysAsnProGluIleValIleTyrGlnTyrMetAspAspLeuTyrValGlySerAsp
ACAAAAAATCCAGAAATAGTCATATACCAATACATGGATGATTTGTATGTAGGGTCTGAT
                                                        2700
LeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGluHisLeuLeuLysTrp
TTAGAAATAGGACAACATAGAACAAAAATAGAGGAACTAAGAGAACATCTATTGAAATGG

GlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyr
GGATTTACCACACCAGACAAAAAGCATCAGAAAGAACCCCCATTTCTTTGGATGGGGTAT
                                    2800
GluLeuHisProAspLysTrpThrValGlnProIleGlnLeuProAspLysGluSerTrp
GAACTGCACCCTGACAAATGGACAGTGCAGCCTATACAACTGCCAGACAAGGAAAGCTGG

ThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIleTyrPro
ACTGTCAATGATATACAGAAATTGGTGGGAAAACTAAATTGGGCAAGTCAGATTTATCCA
            2900
GlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyAlaLysAlaLeuThrAspIle
GGAATTAAAGTAAAGCAATTATGTAAACTCCTTAGGGGAGCAAAAGCACTAACAGACATA
                                                        3000
ValProLeuThrAlaGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGlu
GTACCATTAACTGCAGAGGCAGAATTAGAATTGGCAGAGAACAGGGAAATTCTAAAAGAA
```

FIG. 7D

ProValHisGlyValTyrTyrAspProSerLysAspLeuIleAlaGluIleGlnLysGln
CCAGTGCATGGGGTATATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAG
3100

GlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluGlnTyrLysAsnLeuLysThrGly
GGGCAAGGTCAATGGACATATCAAATATACCAAGAGCAATATAAAAATCTGAAAACAGGG

LysTyrAlaArgIleLysSerAlaHisThrAsnAspValLysGlnLeuThrGluAlaVal
AAGTATGCAAGAATAAAGTCTGCCCACACTAATGATGTAAAACAATTAACAGAAGCAGTG
3200

GlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThrProLysPheArgLeuPro
CAAAAGATAGCCCAAGAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAGACTACCC
3300

IleGlnLysGluThrTrpGluAlaTrpTrpThrGluTyrTrpGlnAlaThrTrpIlePro
ATACAAAAAGAAACATGGGAGGCATGGTGGACAGAATATTGGCAAGCCACCTGGATCCCT

GluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluThrGlu
GAATGGGAGTTTGTCAATACTCCTCCCCTAGTAAAACTATGGTACCAGTTAGAAACAGAA
3400

ProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysLys
CCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGAGAAACTAAAAAG

GlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSerLeuThrGluThr
GGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAGGTTGTCTCCTTAACTGAAACA
3500

ThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspSerGlySerGlu
ACAAATCAGAAGACTGAATTACAAGCAATCCACTTAGCTTTACAGGATTCAGGATCAGAA
3600

ValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLys
GTAAACATAGTAACAGACTCACAGTATGCATTAGGGATTATTCAAGCACAACCAGATAAA

SerGluSerGluIleValAsnGlnIleIleGluGlnLeuIleGlnLysAspLysValTyr
AGTGAATCAGAGATTGTTAATCAAATAATAGAGCAATTAATACAGAAGGACAAGGTCTAC
3700

LeuSerTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnValAspLysLeuVal
CTGTCATGGGTACCAGCACACAAAGGGATTGGAGGAAATGAACAAGTAGATAAATTAGTC

SerSerGlyIleArgLysValLeuPheLeuAspGlyIleAspLysAlaGlnGluGluHis
AGCAGTGGAATCAGAAAGGTACTATTTTTAGATGGGATAGATAAGGCTCAAGAAGAACAT
3800

GluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeuProProIleVal
GAAAAGTATCACAGCAATTGGAGAGCAATGGCTAGTGACTTTAATCTACCACCTATAGTA
3900

AlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGluAlaMetHisGly
GCGAAGGAAATAGTAGCCAGCTGTGATAAATGTCAACTAAAAGGGGAAGCCATGCATGGA

GlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeuGluGlyLysIle
CAAGTAGACTGTAGTCCAGGGATATGGCAATTAGATTGCACACATCTAGAAGGAAAAATA
4000

IleIleValAlaValHisValAlaSerGlyTyrIleGluAlaGluValIleProAlaGlu
ATCATAGTAGCAGTCCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATCCCAGCAGAA

ThrGlyGlnGluThrAlaTyrPheIleLeuLysLeuAlaGlyArgTrpProValLysVal
ACAGGACAGGAGACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTAAAAGTA
4100

FIG. 7E

Val[illegible]rAspAsnGlySerAsnPheThrSerAlaAlaValLysAlaAlaCysTrpTrp
GTACA[illegible]AGACAATGGCAGCAATTTCACCAGTGCTGCAGTTAAAGCAGCCTGTTGGTGG
4200

AlaAsnIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGlnGlyValValGlu
GCAAATATCAAACAGGAATTTGGAATTCCCTACAACCCCCAAAGTCAAGGAGTAGTGGAA

SerMetAsnLysGluLeuLysLysIleIleGlyGlnValArgGluGlnAlaGluHisLeu
TCTATGAATAAGGAATTAAAGAAAATCATAGGGCAGGTAAGAGAGCAAGCTGAACACCTT
4300

LysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLysGlyGlyIleGly
AAGACAGCAGTACAAATGGCAGTGTTCATTCACAATTTTAAAAGAAAAGGGGGGATTGGG

GlyTyrSerAlaGlyGluArgIleIleAspMetIleAlaThrAspIleGlnThrLysGlu
GGGTACAGTGCAGGGGAAAGAATAATAGACATGATAGCAACAGACATACAAACTAAAGAA
4400

LeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArgAspAsnArgAsp
TTACAAAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAGAGAC
4500

ProIleTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAlaValValIleGln
CCAATTTGGAAAGGACCAGCAAAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAG

Q

AspAsnSerAspIleLysValValProArgArgLysAlaLysIleIleArgAspTyrGly
MetGlu
GACAATAGTGATATAAAGGTAGTACCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGA
4600 POL

LysGlnMetAlaGlyAspAspCysValAlaGlyGlyGlnAspGluAsp
AsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIleArgThrTrpHis
AAACAGATGGCAGGTGATGATTGTGTGGCAGGTGGACAGGATGAGGATTAGAACATGGCA

SerLeuValLysHisHisMetTyrValSerLysLysAlaLysAsnTrpPheTyrArgHis
CAGTTTAGTAAAACATCATATGTATGTCTCAAAGAAAGCTAAAAATTGGTTTTATAGACA
4700

HisTyrGluSerArgHisProLysValSerSerGluValHisIleProLeuGlyAspAla
TCACTATGAAAGCAGGCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGGGATGC
4800

ArgLeuValValArgThrTyrTrpGlyLeuGlnThrGlyGluLysAspTrpHisLeuGly
TAGATTAGTAGTAAGAACATATTGGGGTCTGCAAACAGGAGAAAAAGACTGGCACTTGGG

HisGlyValSerIleGluTrpArgGlnLysArgTyrSerThrGlnLeuAspProAspLeu
TCATGGGGTCTCCATAGAATGGAGGCAGAAAAGATATAGCACACAACTAGATCCTGACCT
4900

Al[illegible]pGlnLeuIleHisLeuTyrTyrPheAspCysPheSerGluSerAlaIleArgGln
AGCAGACCAACTGATTCATCTGTACTATTTTGATTGTTTTTCAGAATCTGCCATAAGACA

AlaIleLeuGlyHisIleValSerProArgCysAspTyrGlnAlaGlyHisAsnLysVal
AGCCATATTAGGACATATAGTTAGTCCTAGGTGTGATTATCAAGCAGGACATAACAAGGT
5000

GlySerLeuGlnTyrLeuAlaLeuThrAlaLeuIleAlaProLysLysThrArgProPro
AGGATCTTTACAGTATTTGGCACTAACAGCATTAATAGCACCAAAAAAGACAAGGCCACC
5100

R
MetGluGlnAlaProAlaAspGlnGly
LeuProSerValArgLysLeuThrGluAspArgTrpAsnLysProGlnGlnThrLysGly
TTTGCCTAGTGTTAGGAAGCTAACAGAAGATAGATGGAACAAGCCCCAGCAGACCAAGGG

FIG. 7F

Q

ProGlnArgGluProHisAsnGluTrpThrLeuGluLeuLeuGluGluLeuLysGlnGlu
HisArgGlyS rHisThrMetAsnGlyHis
CCACAGAGGGAGCCACACAATGAATGGACATTAGAACTTTTAGAGGAGCTTAAGCAAGAA
5200

AlaValArgHisPheProArgIleTrpLeuHisSerLeuGlyGlnHisIleTyrGluThr
GCTGTCAGACACTTTCCTAGGATATGGCTCCATAGTTTAGGACAACATATCTATGAAACT

TyrGlyAspThrTrpGluGlyValGluAlaIleIleArgSerLeuGlnGlnLeuLeuPhe
TATGGGGATACCTGGGAAGGAGTTGAAGCTATAATAAGAAGTCTGCAACAACTGCTGTTT
5300

IleHisPheArgIleGlyCysGlnHisSerArgIleGlyIleThrArgGlnArgArgAla
ATTCATTTCAGAATTGGGTGTCAACATAGCAGAATAGGCATTACTCGACAGAGAAGAGCA
5400

S R

ArgAsnGlySerSerArgSer
MetAspProValAspProAsnLeuGluProTrpAsnHisProGlySerGlnProArg
AGAAATGGATCCAGTAGATCCTAACTTAGAGCCCTGGAACCATCCAGGGAGTCAGCCTAG

ThrProCysAsnLysCysTyrCysLysLysCysCysTyrHisCysGlnMetCysPheIle
GACGCCTTGTAATAAGTGTTATTGTAAAAAGTGCTGCTATCATTGCCAAATGTGCTTCAT
5500

ThrLysGlyLeuGlyIleSerTyrGlyArgLysLysArgArgGlnArgArgArgProPro
AACGAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCC

S

GlnGlyAsnGlnAlaHisGlnAspProLeuProGluGln
TCAGGGCAATCAGGCTCATCAAGATCCTCTACCAGAGCAGTAAGTAGTATATGTAATACA
5600

ACCTTTAGTGATATTAGCAATAGTAGCATTAGTAGTAACGCTAATAATAGCAATAGTTGT
5700

GTGGACCATAGTATTTATAGAAATTAGGAAAATAAGAAGACAAAGGAAAATAGACAGGTT

ENV

MetArgValArgGluIleGlnArg
GATTGATAGAATAAGAGAAAGAGCAGAAGATAGTGGCAATGAGAGTGAGGGAGATACAGA
5800

AsnTyrGlnAsnTrpTrpArgTrpGlyMetMetLeuLeuGlyMetLeuMetThrCysSer
GGAATTATCAAAACTGGTGGAGATGGGGCATGATGCTCCTTGGGATGTTGATGACCTGTA

IleAlaGluAspLeuTrpValThrValTyrTyrGlyValProValTrpLysGluAlaThr
GTATTGCAGAAGATTTGTGGGTTACAGTTTATTATGGGGTACCTGTGTGGAAAGAAGCAA
5900

ThrThrLeuPheCysAlaSerAspAlaLysSerTyrGluThrGluValHisAsnIleTrp
CCACTACCCTATTTTGTGCATCAGATGCTAAATCATATGAAACAGAAGTACATAACATCT
6000

AlaThrHisAlaCysValProThrAspProAsnProGlnGluIleGluLeuGluAsnVal
GGGCTACACATGCCTGTGTACCCACGGACCCCAACCCACAAGAAATAGAACTGGAAAATG

ThrGluGlyPheAsnMetTrpLysAsnAsnMetValGluGlnMetHisGluAspIleIle
TCACAGAAGGGTTTAACATGTGGAAAAATAACATGGTGGAGCAGATGCATGAGGATATAA
6100

FIG. 7G

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SerLeuTrpAspGlnSerLeuLysPr CysValLysLeuThrProLeuCysValThrLeu
TCAGTTTATGGGATCAAAGCCTAAAACCATGTGTAAAGCTAACCCCACTCTGTGTCACTT
        .         .         .         .         .         .
AsnCysThrAsnValAsnGlyThrAlaValAsnGlyThrAsnAlaGlySerAsnArgThr
TAAACTGCACTAATGTGAATGGGACTGCTGTGAATGGGACTAATGCTGGGAGTAATAGGA
        .      6200         .         .         .         .
AsnAlaGluLeuLysMetGluIleGlyGluValLysAsnCysSerPheAsnIleThrPro
CTAATGCAGAATTGAAAATGGAAATTGGAGAAGTGAAAAACTGCTCTTTCAATATAACCC
        .         .         .         .         .      6300
ValGlySerAspLysArgGlnGluTyrAlaThrPheTyrAsnLeuAspLeuValGlnIle
CAGTAGGAAGTGATAAAAGGCAAGAATATGCAACTTTTTATAACCTTGATCTAGTACAAA
        .         .         .         .         .         .
AspAspSerAspAsnSerSerTyrArgLeuIleAsnCysAsnThrSerValIleThrGln
TAGATGATAGTGATAATAGTAGTTATAGGCTAATAAATTGTAATACCTCAGTAATTACAC
        .         .         .      6400         .         .
AlaCysProLysValThrPheAspProIleProIleHisTyrCysAlaProAlaGlyPhe
AGGCTTGTCCAAAGGTAACCTTTGATCCAATTCCCATACATTATTGTGCCCCAGCTGGTT
        .         .         .         .         .         .
AlaIleLeuLysCysAsnAspLysLysPheAsnGlyThrGluIleCysLysAsnValSer
TTGCAATTCTAAAGTGTAATGATAAGAAGTTCAATGGAACGGAAATATGTAAAAATGTCA
        .      6500         .         .         .         .
ThrValGlnCysThrHisGlyIleLysProValValSerThrGlnLeuLeuLeuAsnGly
GTACAGTACAATGTACACATGGAATTAAGCCAGTGGTGTCAACTCAACTGCTGTTAAATG
        .         .         .         .         .      6600
SerLeuAlaGluGluGluIleMetIleArgSerGluAsnLeuThrAspAsnThrLysAsn
GCAGTCTAGCAGAAGAAGAGATAATGATTAGATCTGAAAATCTCACAGACAATACTAAAA
        .         .         .         .         .         .
IleIleValGlnLeuAsnGluThrValThrIleAsnCysThrArgProGlyAsnAsnThr
ACATAATAGTACAGCTTAATGAAACTGTAACAATTAATTGTACAAGGCCTGGAAACAATA
        .         .         .      6700         .         .
ArgArgGlyIleHisPheGlyProGlyGlnAlaLeuTyrThrThrGlyIleValGlyAsp
CAAGAAGAGGGATACATTTCGGCCCAGGGCAAGCACTCTATACAACAGGGATAGTAGGAG
        .         .         .         .         .         .
IleArgArgAlaTyrCysThrIleAsnGluThrGluTrpAspLysThrLeuGlnGlnVal
ATATAAGAAGAGCATATTGTACTATTAATGAAACAGAATGGGATAAAACTTTACAACAGG
        .      6800         .         .         .         .
AlaValLysLeuGlySerLeuLeuAsnLysThrLysIleIlePheAsnSerSerSerGly
TAGCTGTAAAACTAGGAAGCCTTCTTAACAAAACAAAAATAATTTTTAATTCATCCTCAG
        .         .         .         .         .      6900
GlyAspProGluIleThrThrHisSerPheAsnCysArgGlyGluPhePheTyrCysAsn
GAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTAGAGGGGAATTTTTCTACTGTA
        .         .         .         .         .         .
ThrSerLysLeuPheAsnSerThrTrpGlnAsnAsnGlyAlaArgLeuSerAsnSerThr
ATACATCAAAACTGTTTAATAGTACATGGCAGAATAATGGTGCAAGACTAAGTAATAGCA
        .         .         .      7000         .         .
GluSerThrGlySerIleThrLeuProCysArgIleLysGlnIleIleAsnMetTrpGln
CAGAGTCAACTGGTAGTATCACACTCCCATGCAGAATAAAACAAATTATAAATATGTGGC
        .         .         .         .         .         .
LysThrGlyLysAlaMetTyrAlaProProIleAlaGlyValIleAsnCysLeuSerAsn
AGAAAACAGGAAAAGCTATGTATGCCCCTCCCATCGCAGGAGTCATCAACTGTTTATCAA
        .      7100         .         .         .         .
IleThrGlyLeuIleLeuThrArgAspGlyGlyAsnSerSerAspAsnSerAspAsnGlu
ATATTACAGGGCTGATATTAACAAGAGATGGTGGAAATAGTAGTGACAATAGTGACAATG
        .         .         .         .         .      7200
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FIG. 7H

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ThrLeuArgPr GlyGlyGlyAspMetArgAspAsnTrpIleSerGluLeuTyrLysTyr
AGACCTTAAGACCTGGAGGAGGAGATATGAGGGACAATTGGATAAGTGAATTATATAAAT

LysValValArgIleGluProLeuGlyValAlaProThrLysAlaLysArgArgValVal
ATAAAGTAGTAAGAATTGAACCCCTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGG
                                7300
GluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeuGlyPheLeuGlyAlaAla
TGGAAAGAGAAAAAAGAGCAATAGGACTAGGAGCCATGTTCCTTGGGTTCTTGGGAGCAG

GlySerThrMetGlyAlaAlaSerLeuThrLeuThrValGlnAlaArgGlnLeuLeuSer
CAGGAAGCACGATGGGCGCAGCGTCACTAACGCTGACGGTACAGGCCAGACAGTTACTGT
     7400
GlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGlnHisLeuLeu
CTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAGGCGCAACAGCATCTGT
                                                        7500
GlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaValGluArgTyr
TGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT

LeuGlnAspGlnArgLeuLeuGlyMetTrpGlyCysSerGlyLysHisIleCysThrThr
ACCTACAGGATCAACGGCTCCTAGGAATGTGGGGTTGCTCTGGAAAACACATTTGCACCA
                                7600
PheValProTrpAsnSerSerTrpSerAsnArgSerLeuAspAspIleTrpAsnAsnMet
CATTTGTGCCTTGGAACTCTAGTTGGAGTAATAGATCTCTAGATGACATTTGGAATAATA

ThrTrpMetGlnTrpGluLysGluIleSerAsnTyrThrGlyIleIleTyrAsnLeuIle
TGACCTGGATGCAGTGGGAAAAAGAAATTAGCAATTACACAGGCATAATATACAACTTAA
     7700
GluGluSerGlnIleGlnGlnGluLysAsnGluLysGluLeuLeuGluLeuAspLysTrp
TTGAAGAATCGCAAATCCAGCAAGAAAAGAATGAAAAGGAATTATTGGAATTGGACAAGT
                                                        7800
AlaSerLeuTrpAsnTrpPheSerIleSerLysTrpLeuTrpTyrIleArgIlePheIle
GGGCAAGTTTGTGGAATTGGTTTAGCATATCAAAATGGCTGTGGTATATAAGAATATTCA

IleValValGlyGlyLeuIleGlyLeuArgIleIlePheAlaValLeuSerLeuValAsn
TAATAGTAGTAGGAGGCTTAATAGGTTTAAGAATAATTTTTGCTGTGCTTTCTTTAGTAA
                                7900
ArgValArgGlnGlyTyrSerProLeuSerLeuGlnThrLeuLeuProThrProArgGly
ATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTGCAGACCCTCCTCCCAACACCGAGGG

ProProAspArgProGluGlyIleGluGluGlyGlyGluGlnGlyArgGlyArgSer
GACCACCCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGCAAGGCAGAGGCAGAT
     8000
IleArgLeuValAsnGlyPheSerAlaLeuIleTrpAspAspLeuArgAsnLeuCysLeu
CAATTCGATTGGTGAACGGATTCTCAGCACTTATCTGGGACGACCTGAGGAACCTGTGCC
                                                        8100
PheSerTyrHisArgLeuArgAspLeuLeuLeuIleAlaThrArgIleValGluLeuLeu
TCTTCAGTTACCACCGCTTGAGAGACTTACTCTTAATTGCAACGAGGATTGTGGAACTTC

GlyArgArgGlyTrpGluAlaLeuLysTyrLeuTrpAsnLeuLeuGlnTyrTrpGlyGln
TGGGACGCAGGGGGTGGGAAGCCCTCAAATATCTGTGGAATCTCCTGCAATATTGGGGTC
                                8200
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FIG. 7I

GluLeuLysAsnSerAlaIleSerLeuLeuAsnThrThrAlaIleAlaValAlaGluCys
AGGAACTGAAGAATAGTGCTATTAGCTTGCTTAATACCACAGCAATAGCAGTAGCTGAAT

ThrAspArgValIleGluIleGlyGlnArgPheGlyArgAlaIleLeuHisIleProArg
GCACAGATAGGGTTATAGAAATAGGACAAAGATTTGGTAGAGCTATTCTCCACATACCTA
8300

EW ← F → MetGlyGlyLysTrpSerLys
ArgIleArgGlnGlyPheGluArgAlaLeuLeu
GAAGAATTAGACAGGGCTTCGAAAGGGCTTTGCTATAACATGGGTGGCAAGTGGTCAAAA
8400

SerSerIleValGlyTrpProLysIleArgGluArgIleArgArgThrProProThrGlu
AGTAGCATAGTAGGATGGCCTAAGATTAGGGAAAGAATAAGACGAACTCCCCCAACAGAA

ThrGlyValGlyAlaValSerGlnAspAlaValSerGlnAspLeuAspLysCysGlyAla
ACAGGAGTAGGAGCAGTATCTCAAGATGCAGTATCTCAAGATTTAGATAAATGTGGAGCA
8500

AlaAlaSerSerSerProAlaAlaAsnAsnAlaSerCysGluProProGluGluGluGlu
GCCGCAAGCAGCAGTCCAGCAGCTAATAATGCTAGTTGTGAACCACCAGAAGAAGAGGAG

GluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLysGlyAla
GAGGTAGGCTTTCCAGTCCGTCCTCAGGTACCTTTAAGACCAATGACTTATAAAGGAGCT
8600

→U3
PheAspLeuSerHisPheLeuLysGluLysGlyGlyLeuAspGlyLeuValTrpSerPro
TTTGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGATGGGTTAGTTTGGTCCCCA
8700

LysArgGlnGluIleLeuAspLeuTrpValTyrHisThrGlnGlyTyrPheProAspTrp
AAAAGACAAGAAATCCTTGATCTGTGGGTCTACCACACACAAGGCTACTTCCCTGATTGG

GlnAsnTyrThrProGlyProGlyIleArgPheProLeuThrPheGlyTrpCysPheLys
CAGAATTACACACCAGGGCCAGGGATTAGATTCCCACTGACCTTCGGATGGTGCTTTAAG
8800

LeuValProMetSerProGluGluValGluGluAlaAsnGluGlyGluAsnAsnCysLeu
TTAGTACCAATGAGTCCAGAGGAAGTAGAGGAGGCCAATGAAGGAGAGAACAACTGTCTG

LeuHisProIleSerGlnHisGlyMetGluAspAlaGluArgGluValLeuLysTrpLys
TTACACCCTATTAGCCAACATGGAATGGAGGACGCAGAAAGAGAAGTGCTAAAATGGAAG
8900

PheAspSerSerLeuAlaLeuArgHisArgAlaArgGluGlnHisProGluTyrTyrLys
TTTGACAGCAGCCTAGCACTAAGACACAGAGCCAGAGAACAACATCCGGAGTACTACAAA
9000

F ←
AspCys
GACTGCTGACACAGAAGTTGCTGACAGGGGACTTTCCGCTGGGGACTTTCCAGGGGAGGC

GTAACTTGGGCGGGACCGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGCTGCTT
9100

U3 ← → R
TTCGCCTGTACTGGGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGC

AAGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAA
9200